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OM protein - protein search, using SW model

Run on: June 18, 2002, 14:55:49 ; Search time 13.05 seconds
(without alignment)
475,410 Million cell updates/sec

Title: US-09-788-626-2

Perfect score: 1147

Sequence: 1 THICKVAKLFFRRKRENYR

Scoring table: BLOSUM62

Gapop: 10.0, Gapext: 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued: Patents-AA*

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13: /cgn2_6/prodata/2/1aa/6L_COMB.pep.*

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15: /cgn2_6/prodata/2/1aa/6N_COMB.pep.*

16: /cgn2_6/prodata/2/1aa/6O_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	99.2	320	US-09-964-308-2	Sequence 2, Appl 1
2	1336	99.2	320	US-08-964-313-2	Sequence 2, Appl 1
3	1336	99.2	320	US-09-069-138-2	Sequence 2, Appl 1
4	1336	99.2	385	US-08-036-210-5	Sequence 5, Appl 1
5	1336	99.2	385	US-08-449-609-5	Sequence 8, Appl 1
6	1314.5	97.6	322	US-08-964-313-8	Sequence 8, Appl 1
7	1314.5	97.6	322	US-09-069-138-8	Sequence 8, Appl 1
8	1314.5	97.6	322	US-08-685-992-1	Sequence 1, Appl 1
9	1060	78.7	196	US-08-144-925-1	Sequence 1, Appl 1
10	1060	78.7	196	US-09-144-925-1	Sequence 2, Appl 1
11	811	60.2	134	US-08-685-992-2	Sequence 2, Appl 1
12	811	60.2	134	US-09-144-925-2	Sequence 2, Appl 1
13	616	45.7	120	US-08-449-609-5	Sequence 2, Appl 1
14	508.5	37.0	278	US-08-201-697-16	Sequence 17, Appl 1
15	498.5	37.0	254	US-08-685-992-14	Sequence 14, Appl 1
16	498.5	37.0	254	US-09-144-925-14	Sequence 14, Appl 1
17	490	36.4	273	US-08-201-697-17	Sequence 17, Appl 1
18	484.5	36.0	251	US-08-685-992-15	Sequence 15, Appl 1
19	484.5	36.0	251	US-09-144-925-15	Sequence 15, Appl 1
20	481	35.7	257	US-08-685-992-6	Sequence 6, Appl 1
21	481	35.7	257	US-09-144-925-6	Sequence 6, Appl 1
22	478.5	35.5	285	US-08-685-992-12	Sequence 12, Appl 1
23	478.5	35.5	285	US-09-144-925-12	Sequence 12, Appl 1
24	474	35.2	1337	US-08-685-992-2	Sequence 2, Appl 1
25	474	35.2	1337	PCT US95-05512-2	Sequence 2, Appl 1
26	473.5	35.2	263	US-08-685-992-5	Sequence 5, Appl 1
27	473.5	35.2	263	US-09-144-925-5	Sequence 5, Appl 1

28	471.5	35.0	1501	2	US-08-447-464-3	Sequence 3, Appl 1
29	471.5	35.0	1501	2	US-08-716-679-3	Sequence 3, Appl 1
30	469	34.8	258	2	US-08-685-992-19	Sequence 19, Appl 1
31	469	34.8	258	2	US-09-144-925-19	Sequence 19, Appl 1
32	468.5	34.6	593	1	US-08-202-389-12	Sequence 12, Appl 1
33	468.5	34.6	250	2	US-08-685-992-7	Sequence 7, Appl 1
34	466.5	34.6	250	2	US-09-144-925-7	Sequence 7, Appl 1
35	464.5	34.5	1445	1	US-08-447-464-2	Sequence 2, Appl 1
36	464.5	34.5	1445	1	US-08-348-0068-5	Sequence 5, Appl 1
37	464.5	34.5	1911	2	US-08-800-825A-5	Sequence 5, Appl 1
38	464.5	34.5	1911	2	US-08-800-825A-5	Sequence 5, Appl 1
39	464.5	34.5	1911	2	US-09-158-657-5	Sequence 5, Appl 1
40	464.5	34.5	1911	5	PCT-US94-10166-5	Sequence 5, Appl 1
41	463.5	34.4	593	1	US-08-018-129-5	Sequence 5, Appl 1
42	463.5	34.4	593	2	US-08-448-450-5	Sequence 5, Appl 1
43	461.5	34.3	1442	1	US-08-015-986A-3	Sequence 3, Appl 1
44	461.5	34.3	1442	2	US-08-446-363-3	Sequence 3, Appl 1
45	460	34.1	1188	1	US-08-201-697-4	Sequence 4, Appl 1

ALIGNMENTS

RESULT 1
US-08-964-308-2
Sequence 2, Application US/089644108
Patent No. 6066715
GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: PRIESTEN, RICHARD
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: ROBERT J. NORTH - MERCK & CO., INC.
STREET: 124 EAST LINTON AVENUE - P.O. BOX 2000
CITY: RANNEY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
OPERATING SYSTEM: IBM PC Compatible
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,308
FILING DATE: 04-Nov-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: 19840 PCT
TELEPHONE: 732-594-7262
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-308-2
Query Match 99.2% Score 1336; DB 3; Length 320;
Best Local Similarity 99.2% Pred No. 8 40-135;
Matches 254; Gaps 0; Inbols 2; Gaps 1;
UY 1 DFCQVAKLPKNNRRNYKDVSPHDSRIKLHOFNDYINASIIMKRIAGRSYIITQGM. 60

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14 DEPRVAKLKKNNKNNRYKVSIPDHSRIKJHQBNDYINASTLIMLAQSYLLUGPL 88
QY 29 PNTGHHFWMMWOKSRVVMNLNRYMEKSKLCAQYWPQKEEEMTEETNLKTLISED 120
149 IKSYTVBQLEENLTGTRETIHFHTTWDPGVPESPASFLNPLKVRSSLSPEH 178
149 IKSYTVBQLEENLTGTRETIHFHTTWDPGVPESPASFLNPLKVRSSLSPEH 208
QY 121 IKSYTV--LELENLTGTRETIHFHTTWDPGVPESPASFLNPLKVRSSLSPEH 178
149 IKSYTVBQLEENLTGTRETIHFHTTWDPGVPESPASFLNPLKVRSSLSPEH 208
DB 89 PNTGHHFWMMWOKSRVVMNLNRYMEKSKLCAQYWPQKEEEMTEETNLKTLISED 148
QY 179 GPVVVHSGAGISGSGTFLADPCLIMKPKDPSVDIKKVLLEMKKPMCLJOTADQUR 238
DB 209 GPVVVHSGAGISGSGTFLADPCLIMKPKDPSVDIKKVLLEMKKPMCLJOTADQUR 268
QY 239 FSYLAVIEGAKFIMCD 254
DB 269 FSYLAVIEGAKFIMCD 284

RESULT 2
US-09-964-413-2
Sequence 2: Application US/09964-413
Patent No. 6114142
GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: GRESSER, MICHAEL
APPLICANT: KENNEDY, BRIAN
APPLICANT: NICHOLSON, DONALD
APPLICANT: KAMACHANON, CHIDAMARAN
APPLICANT: SKOREY, KATHRYN
APPLICANT: FORD JOTHINSON, ANTHONY
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILIPPE L. DURETTE, MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/094964-413
FILING DATE: 04 NOV 1997
CLASSIFICATION: 455
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/010,408
FILING DATE: 04 NOV 1996
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/97/090825
FILING DATE: 04 NOV 1996
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 45,125
REFERENCE/DOCKET NUMBER: 19824Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-964-413-2

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Query Match          99.2% Score 1346; DB 3; Length 420;
Best Local Similarity 99.2% Pred. No. 8,3e 15;
Matches 254; Conserved 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DPGVAKLKKNNKNNRYKVSIPDHSRIKJHQBNDYINASTLIMLAQSYLLUGPL 60
DB 29 DPGVAKLKKNNKNNRYKVSIPDHSRIKJHQBNDYINASTLIMLAQSYLLUGPL 88
QY 61 PNTGHHFWMMWOKSRVVMNLNRYMEKSKLCAQYWPQKEEEMTEETNLKTLISED 120
DB 89 PNTGHHFWMMWOKSRVVMNLNRYMEKSKLCAQYWPQKEEEMTEETNLKTLISED 148
QY 121 IKSYTV--LELENLTGTRETIHFHTTWDPGVPESPASFLNPLKVRSSLSPEH 178
DB 149 IKSYTVBQLEENLTGTRETIHFHTTWDPGVPESPASFLNPLKVRSSLSPEH 208
QY 179 GPVVVHSGAGISGSGTFLADPCLIMKPKDPSVDIKKVLLEMKKPMCLJOTADQUR 238
DB 209 GPVVVHSGAGISGSGTFLADPCLIMKPKDPSVDIKKVLLEMKKPMCLJOTADQUR 268
QY 239 FSYLAVIEGAKFIMCD 254
DB 269 FSYLAVIEGAKFIMCD 284

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RESULT 3
US-09-069-138-2
Sequence 2: Application US/09069-138
Patent No. 6,448,572
GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, CLAUDE
APPLICANT: FRIESEN, RICHARD
APPLICANT: LEBLANC, YVES
APPLICANT: ROY, PATRICK
APPLICANT: YOUNG, ROBERT N.
APPLICANT: ZAMRONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILIPPE L. DURETTE, MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISKETTE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,138
FILING DATE: 29 APR 1998
CLASSIFICATION: 540
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19840Y1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-069-138-2

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Query Match 99.2% Score 1336; DB 4; Length 320.
Best Local Similarity 99.2% Pred No. 8.36-135;
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DEPRVAKLPKNNRNRYRVSPFDHSRIKIHQEDNDYINASTIKMEFAORSYITGGPL 60
DB 23 DEPRVAKLPKNNRNRYRVSPFDHSRIKIHQEDNDYINASTIKMEFAORSYITGGPL 88
QY 61 PNTGHEWENWEDKSGVYMLNRYMEKSLKCAQYWPQKEKEMIFEDTNLKLTLISED 120
DB 89 PNTGHEWENWEDKSGVYMLNRYMEKSLKCAQYWPQKEKEMIFEDTNLKLTLISED 148
QY 121 IKSYTV--TELENTTQETRELIHFHYTTWPCFVTEFASPLNLFKVRSGSLSPH 178
DB 149 IKSYTVQULENLITJQETRELIHFHYTTWPCFVTEFASPLNLFKVRSGSLSPH 208
QY 179 GPVVVHCAGIGRGTCTADTCLLMKRRKDPSSVDIKKVLLEMRKFMGLIOTADQLR 238
DB 209 GPVVVHCAGIGRGTCTADTCLLMKRRKDPSSVDIKKVLLEMRKFMGLIOTADQLR 268
QY 239 FSYLAVIEGAKFTMGD 254
DB 269 FSYLAVIEGAKFTMGD 284

RESULT 4
US-08-036-210-5
Sequence 5, Application US/08036210
Patent No. 5585233
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SKO ID NO: 5;
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-036-210-5

Query Match

99.2% Score 1336; DB 1; Length 385;

Best Local Similarity 99.2% Pred No. 1.1e-134;
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DEPRVAKLPKNNRNRYRVSPFDHSRIKIHQEDNDYINASTIKMEFAORSYITGGPL 60
DB 23 DEPRVAKLPKNNRNRYRVSPFDHSRIKIHQEDNDYINASTIKMEFAORSYITGGPL 88
QY 61 PNTGHEWENWEDKSGVYMLNRYMEKSLKCAQYWPQKEKEMIFEDTNLKLTLISED 120
DB 89 PNTGHEWENWEDKSGVYMLNRYMEKSLKCAQYWPQKEKEMIFEDTNLKLTLISED 148
QY 121 IKSYTV--TELENTTQETRELIHFHYTTWPCFVTEFASPLNLFKVRSGSLSPH 178
DB 149 IKSYTVQULENLITJQETRELIHFHYTTWPCFVTEFASPLNLFKVRSGSLSPH 208
QY 179 GPVVVHCAGIGRGTCTADTCLLMKRRKDPSSVDIKKVLLEMRKFMGLIOTADQLR 238
DB 209 GPVVVHCAGIGRGTCTADTCLLMKRRKDPSSVDIKKVLLEMRKFMGLIOTADQLR 268
QY 239 FSYLAVIEGAKFTMGD 254
DB 269 FSYLAVIEGAKFTMGD 284

RESULT 5
US-08-449-609-5
Sequence 5, Application US/08449609
Patent No. 5552212
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SKO ID NO: 5;
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-449-609-5

Query Match

99.2% Score 1336; DB 2; Length 385;

Best local similarity 99.2% Prod. No. 1-10-134
 Matches 243 Conserved 0 Mismatches 0 Indels 2 Gaps 1

QY 1 DEPCVAKIKRNNNNRYVSPFQSPRIKIHQEDINYNINSLIKMEFAKSYLLIQGL 60
 DB 29 DPICVAVAKLRNNNNRYVSPFQSPRIKIHQEDINYNINSLIKMEFAKSYLLIQGL 88
 QY 61 PNICGHFWMEWQSKGVMLNPKVFKGSI KCAQYWPQKEKEMIFEDINIKLILSED 120
 DB 89 PNICGHFWMEWQSKGVMLNPKVFKGSI KCAQYWPQKEKEMIFEDINIKLILSED 148
 QY 121 IKSYIV--LEENITLQETRELLHFHTWDPGVPSFASPLNLFVRESGSLSPH 178
 DB 149 IKSYIVKQLEENITLQETRELLHFHTWDPGVPSFASPLNLFVRESGSLSPH 208
 QY 179 GPVYVHSSAGICTGCRSGTFCIADICLLMKRKDPSSVDIKKVLLEKRFKMGILQTAD 238
 DB 209 GPVYVHSSAGICTGCRSGTFCIADICLLMKRKDPSSVDIKKVLLEKRFKMGILQTAD 268
 QY 236 QLRPSYLAIVEGAKFIMGD 254
 DB 269 QLRPSYLAIVEGAKFIMGD 287

RESULT 6
 US-08-964-408-8
 Sequence 8, Application US/08964408
 Patent No. 6066715
 GENERAL INFORMATION:
 APPLICANT: DESMARAIS, SYLVIE
 APPLICANT: FRIESEN, RICHARD
 APPLICANT: KENNEDY, BRIAN
 APPLICANT: NICHOLSON, DONALD
 APPLICANT: RAMACHANDRAN, CHIDAMBARAN
 APPLICANT: SKOREY, KATHRYN
 APPLICANT: FORD-HUTCHINSON, ANTHONY
 TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
 STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 CITY: RAHWAY
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/964,408
 FILING DATE: 04 NOV 1996
 CLASSIFICATION: 540
 ATTORNEY/AGENT INFORMATION:
 NAME: NORTH ROBERT J
 REGISTRATION NUMBER: 27,466
 REFERENCE/DOCKET NUMBER: 19840 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 732-594-7262
 TELEFAX: 732-594-4720
 INDEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 422 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MULTIPLE TYPE: peptide
 US-08-964-408-8

Query Match 99.2% Score 114.59 DB 1 Length 322
 Best local similarity 99.7% Prod. No. 1-70-142
 Matches 253 Conserved 10 Mismatches 1 Indels 5 Gaps 2

QY 1 DEPCVAKIKRNNNNRYVSPFQSPRIKIHQEDINYNINSLIKMEFAKSYLLIQGL 60
 DB 29 DPICVAVAKLRNNNNRYVSPFQSPRIKIHQEDINYNINSLIKMEFAKSYLLIQGL 88
 QY 61 PNICGHFWMEWQSKGVMLNPKVFKGSI KCAQYWPQKEKEMIFEDINIKLILSED 120
 DB 89 PNICGHFWMEWQSKGVMLNPKVFKGSI KCAQYWPQKEKEMIFEDINIKLILSED 148
 QY 121 IKSYIV--LEENITLQETRELLHFHTWDPGVPSFASPLNLFVRESGSLSPH 178
 DB 149 IKSYIVKQLEENITLQETRELLHFHTWDPGVPSFASPLNLFVRESGSLSPH 208
 QY 179 GPVYVHSSAGICTGCRSGTFCIADICLLMKRKDPSSVDIKKVLLEKRFKMGILQTAD 238
 DB 209 GPVYVHSSAGICTGCRSGTFCIADICLLMKRKDPSSVDIKKVLLEKRFKMGILQTAD 268
 QY 236 QLRPSYLAIVEGAKFIMGD 254
 DB 269 QLRPSYLAIVEGAKFIMGD 287

RESULT 7
 US-08-964-313-8
 Sequence 8, Application US/08964413
 Patent No. 6114132
 GENERAL INFORMATION:
 APPLICANT: DESMARAIS, SYLVIE
 APPLICANT: FRIESEN, RICHARD
 APPLICANT: GRESSER, MICHAEL
 APPLICANT: KENNEDY, BRIAN
 APPLICANT: NICHOLSON, DONALD
 APPLICANT: RAMACHANDRAN, CHIDAMBARAN
 APPLICANT: SKOREY, KATHRYN
 APPLICANT: FORD-HUTCHINSON, ANTHONY
 TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
 STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 CITY: RAHWAY
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/964,313
 FILING DATE: 04 NOV 1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/040,408
 FILING DATE: 04 NOV 1996
 APPLICATION NUMBER: PCT/CA97/00825
 FILING DATE: 03 NOV 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: DURETTE, PHILIPPE L.
 REGISTRATION NUMBER: 35,125
 REFERENCE/DOCKET NUMBER: 19824Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 732-594-4568
 TELEFAX: 732-594-4720
 INDEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 322 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-964-313-8

Query Match 97.6% Score 1314.5; DB 3; Length 322;
 Host Local Similarity 97.7% Prod. No. 1.76-132;
 Matches 253; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

QY 1 DEPCVAKIPKRNKRNRYRSPEDHSPIKLIHQENDYINASTIKMEEAQRSYILTGPL 60
 |||||||
 DB 29 DEPCVAKIPKRNKRNRYRSPEDHSPIKLIHQENDYINASTIKMEEAQRSYILTGPL 88
 QY 61 PNTGCHFWEMWEEKSRGVVMIINVMKESLKCQAYWPKREKEMIFEDTNLKLTLISED 120
 |||||||
 DB 89 PNTGCHFWEMWEEKSRGVVMIINVMKESLKCQAYWPKREKEMIFEDTNLKLTLISED 148
 QY 121 IKSYYTV--LELENLTQFERELLHAFHYTMDPGVPSPASPLNPLPKVRESGLSPRH 178
 |||||||
 DB 149 IKSYYTVHOLELNTLTQFERELLHAFHYTMDPGVPSPASPLNPLPKVRESGLSPRH 208
 QY 179 GIVVHSSAGI--GRSITFLATPILLMFKRPSVDIKVLLPKRPFMGITOTAD 235
 |||||||
 DB 209 GIVVHSSAGI--GRSITFLATPILLMFKRPSVDIKVLLPKRPFMGITOTAD 268
 QY 236 QLETSYLAIVIEGAKFTMGD 254
 |||||||
 DB 269 QLETSYLAIVIEGAKFTMGD 287

RESULT 8
 US-09-069-138-8
 ? Sequence 8, Application US/09069138
 ? Patent No. 6348572
 ? GENERAL INFORMATION:
 ? APPLICANT: DESMARAIS, STEPHIE
 ? APPLICANT: DUFRESNE, CLAUDE
 ? APPLICANT: FRIESEN, RICHARD
 ? APPLICANT: LERLANG, YVES
 ? APPLICANT: ROY, PATRICK
 ? APPLICANT: YOUNG, ROBERT N.
 ? APPLICANT: ZAMHONI, ROBERT
 ? TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
 ? TITLE OF INVENTION: BINDING ASSAY
 ? NUMBER OF SEQUENCES: 15
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
 ? STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 ? CITY: RAHWAY
 ? STATE: NJ
 ? COUNTRY: USA
 ? ZIP: 07065
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy Diskette
 ? COMPUTER: IBM PC Compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: FASTSEQ for Windows Version 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/069,138
 ? FILING DATE: 29-APR-1998
 ? CLASSIFICATION: 530
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: DURETTE, PHILIPPE L.
 ? REGISTRATION NUMBER: 35,125
 ? REFERENCE/DOCKET NUMBER: 19840YIA
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 732-594-4568
 ? TELEFAX: 732-594-4720
 ? TELEX:
 ? INFORMATION FOR SEQ ID NO: 8:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 322 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide

US-09-069-138-8

Query Match 97.6% Score 1314.5; DB 4; Length 322;
 Host Local Similarity 97.7% Prod. No. 1.76-132;
 Matches 253; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

QY 1 DEPCVAKIPKRNKRNRYRSPEDHSPIKLIHQENDYINASTIKMEEAQRSYILTGPL 60
 |||||||
 DB 29 DEPCVAKIPKRNKRNRYRSPEDHSPIKLIHQENDYINASTIKMEEAQRSYILTGPL 88
 QY 61 PNTGCHFWEMWEEKSRGVVMIINVMKESLKCQAYWPKREKEMIFEDTNLKLTLISED 120
 |||||||
 DB 89 PNTGCHFWEMWEEKSRGVVMIINVMKESLKCQAYWPKREKEMIFEDTNLKLTLISED 148
 QY 121 IKSYYTV--LELENLTQFERELLHAFHYTMDPGVPSPASPLNPLPKVRESGLSPRH 178
 |||||||
 DB 149 IKSYYTVHOLELNTLTQFERELLHAFHYTMDPGVPSPASPLNPLPKVRESGLSPRH 208
 QY 179 GIVVHSSAGI--GRSITFLATPILLMFKRPSVDIKVLLPKRPFMGITOTAD 235
 |||||||
 DB 209 GIVVHSSAGI--GRSITFLATPILLMFKRPSVDIKVLLPKRPFMGITOTAD 268
 QY 236 QLETSYLAIVIEGAKFTMGD 254
 |||||||
 DB 269 QLETSYLAIVIEGAKFTMGD 287

RESULT 9
 US-08-685-992-1
 ? Sequence 1, Application US/08068992
 ? Patent No. 5912138
 ? GENERAL INFORMATION:
 ? APPLICANT: Tonks, Nicholas
 ? APPLICANT: Flint, Andrew J.
 ? TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ? TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ? NUMBER OF SEQUENCES: 36
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: HAMPTON, BROOK, SMITH & KYNOLDS, P.C.
 ? STREET: TWO MILLITIA DRIVE
 ? CITY: Lexington
 ? STATE: MA
 ? COUNTRY: USA
 ? ZIP: 02173
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: Windows 95
 ? SOFTWARE: FASTSEQ for Windows Version 2.0b
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/068,992
 ? FILING DATE: 25-JUL-1996
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER:
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Granahan, Patricia
 ? REGISTRATION NUMBER: 32,237
 ? REFERENCE/DOCKET NUMBER: CSHL96-03
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 781-861-6240
 ? TELEFAX: 781-861-9540
 ? TELEX:
 ? INFORMATION FOR SEQ ID NO: 1:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 196 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? US-08-685-992-1

Query Match 78.7%; Score 1060; DB 2; Length 196;
 Best Local Similarity 100.0%; Filed No. 1.3e-105;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPCGVAKLKKNNKNNRVSPFDSIRIKLHQEDNDYINASTLKMEFAQSYLLTQGPL 60
 DB 1 DPCGVAKLKKNNKNNRVSPFDSIRIKLHQEDNDYINASTLKMEFAQSYLLTQGPL 60

QY 61 PNTGHHWEMWEGSKSGVYVNLNVMKSGSLKQVWPFQKEKEMIFEDTNKLTLLSED 120
 DB 61 PNTGHHWEMWEGSKSGVYVNLNVMKSGSLKQVWPFQKEKEMIFEDTNKLTLLSED 120

QY 121 IKSYIVLELENTLTQETRELFHHTTWDPGVESFASPLNLFKVRSGSLSPHP 180
 DB 121 IKSYIVLELENTLTQETRELFHHTTWDPGVESFASPLNLFKVRSGSLSPHP 180

QY 181 VVWHSAGIGSGTEG 196
 DB 181 VVWHSAGIGSGTEG 196

RESULT 11
 US-09-144-925-1
 Sequence 1; Application US/09144925
 Patent No. 5951979
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 APPLICANT: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Millia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02421-1799
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: IBM Compatible
 SOFTWARE: FastSeq for Windows Version 2.0b
 APPLICATION NUMBER: US/09/144,925
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Grahman, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHU-96-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-9240
 TELEFAX: 781-861-9240
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 196 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-144-925-1

Query Match 78.7%; Score 1060; DB 2; Length 196;
 Best Local Similarity 100.0%; Filed No. 1.3e-105;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPCGVAKLKKNNKNNRVSPFDSIRIKLHQEDNDYINASTLKMEFAQSYLLTQGPL 60
 DB 1 DPCGVAKLKKNNKNNRVSPFDSIRIKLHQEDNDYINASTLKMEFAQSYLLTQGPL 60

QY 61 PNTGHHWEMWEGSKSGVYVNLNVMKSGSLKQVWPFQKEKEMIFEDTNKLTLLSED 120
 DB 61 PNTGHHWEMWEGSKSGVYVNLNVMKSGSLKQVWPFQKEKEMIFEDTNKLTLLSED 120

QY 121 IKSYIVLELENTLTQETRELFHHTTWDPGVESFASPLNLFKVRSGSLSPHP 180
 DB 121 IKSYIVLELENTLTQETRELFHHTTWDPGVESFASPLNLFKVRSGSLSPHP 180

QY 181 VVWHSAGIGSGTEG 196
 DB 181 VVWHSAGIGSGTEG 196

RESULT 11
 US-08-685-992-2
 Sequence 2; Application US/08685992
 Patent No. 5912138
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 APPLICANT: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Millia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: IBM Compatible
 SOFTWARE: FastSeq for Windows Version 2.0b
 APPLICATION NUMBER: US/08/685,992
 FILING DATE: 25-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Grahman, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHU-96-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 194 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-685-992-2

Query Match 60.2%; Score 811; DB 2; Length 194;
 Best Local Similarity 74.8%; Filed No. 5.5e-79;
 Matches 144; Conservative 29; Mismatches 29; Indels 2; Gaps 2;

QY 1 DPCGVAKLKKNNKNNRVSPFDSIRIKLHQEDNDYINASTLKMEFAQSYLLTQGPL 60
 DB 1 DPCGVAKLKKNNKNNRVSPFDSIRIKLHQEDNDYINASTLKMEFAQSYLLTQGPL 59

THE UNIVERSITY OF CHICAGO

Sequence 16, APPLICATION US/
 Patent No. 5705623

; Sequence ID, APPLICATION US/2013/010333
; Patent NO. 5705623

1 COUNTRY: USA
 2 ZIP: 02173
 3
 4 COMPUTER READABLE FORM:
 5 MEDIUM TYPE: Diskette
 6 COMPUTER: IBM Compatible
 7 OPERATING SYSTEM: Windows 95
 8 SOFTWARE: FASTSO for Windows Version 2.0b
 9
 10 CURRENT APPLICATION DATA:
 11 APPLICATION NUMBER: US/08/685,992
 12 FILING DATE: 25-JUL-1996
 13 CLASSIFICATION: 435
 14
 15 PRIOR APPLICATION DATA:
 16 APPLICATION NUMBER:
 17 FILING DATE:
 18
 19 ATTORNEY/AGENT INFORMATION:
 20 NAME: Granahan, Patricia
 21 REGISTRATION NUMBER: 32,227
 22 REFERENCE/DOCKET NUMBER: TSH196-03
 23 TELECOMMUNICATION INFORMATION:
 24 TELEPHONE: 781-861-6240
 25 TELEFAX: 781-861-9540
 26
 27 TELEX:
 28
 29 INFORMATION FOR SEQ ID NO: 14:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 254 amino acids
 32 TYPE: amino acid
 33 STRANDEDNESS: single
 34 TOPOLOGY: linear
 35
 36 MOLECULE TYPE: peptide
 37
 38 US-08-685-992-14

QY	4	GRVAKLPPKKNNRRKRYKIVSPHDSHFKLHNDP---	NIYINASHLKKHFFQDSHVIHQG	59
Db	4	GDIALLPENRGRKKRYNNILPVDATRKVLNSVDDPDSQDIYINASTPQNNFRRELYITQAP		63
QY	60	LRPTGCHFFMYVMEKSPGVVMLNVVMKSGKLVQVWPVKEEEMFEETNKLKLILSE		119
Db	64	LPRTGCHFFMYVMEKSPGVVMLNVVMKSGKLVQVWPVKEEEMFEETNKLKLILSE		120
QY	120	DIKSYSTVLEL--ENIITQETRPILNHYTTPDPGVSPENSPASFLNPLRKEVSQSLSP		176
Db	121	SVLPEDMTIFKIGGEEDLDAN--RLIRNHYVVMDDHGVSEFTQSLIQFVRYTVINRSE		178
QY	177	EHGVVWVWFSAGIGSPGSPCLANVCLILMDPKKIDSSVDIKKVLLEPKKRNHGLQIAUD		216
Db	179	GAHPVTVWFSAGVSGPTGTALNPLTLEDPGR--DSVDIGVNHGLLELRIMVQGL--E		218
QY	237	LRSTYL	242	
Db	234	QGVTVL	239	

Search completed: June 18, 2002, 14:56:12
Job time: 23 sec

Matches 254: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEPCRVAKLIPKNNKNNRYRVSPEHDSRIKIHQEDNDYINASLIMKFAQASYLTGQPL 60
 DB 1 dipcrvaklprknknrrydrvspsidhsrikihqedndyinaslkmwaaqsylltqpl 60
 QY 61 PNTGHEHEWMEWEEKSRGVMLNRYMEKGSILKAYWPFQKEEKMEFEEDNLKLTISED 120
 DB 61 pntghehewmeeweksrqvmnlrvmecksgilkaaywfpqkeekmefednlklitised 120
 QY 121 IKSYYTV--LELENTTQETREILHFHYTTPDQVPESPASFLNPLFKVRESGSLSPEN 180
 DB 121 lksyytvleleenttqetrelhfhyytwpdqvpespasflnplfkvresgslspen 180
 QY 181 VVHVCAGICRSCFPLADICILIMKKKQSSVDIKKYLIMRKPRMCLIGTAQOLR 240
 DB 181 vvvhcagiqrsctfpladrcilimkkqssvdiikkylimrkprmclicgtaqolr 240
 QY 241 YLAVIEGAKPTMGD 254
 DB 241 ylaviegaktimgd 254

RESULT 3
 AAR13907
 ID AAR13907 standard; Protein: 435 AA.

XX AC AAR13907;
 XX DT 28-NOV-1991 (first entry)
 XX DE Human protein phosphotyrosyl phosphatase PTPB.
 XX KW PTPase B1; growth suppression activity; ANL; myeloproliferation.
 XX OS Homo sapiens.
 XX FN W09113173-A.
 XX PD 05-SEP-1991.
 XX PF 01-MAR-1991; 91WO-0001432.
 XX ER 18-JAN-1991; 91US-0643041.
 XX PR 02-MAR-1990; 90US-0487733.
 XX PA (B107-) APPL BIOTECHN INC.
 XX PI Bruskin AM, Hill DE;
 XX DR WPI: 1991-281485/38.
 XX N-INDB: AAN13643.
 XX PT Vector contg. protein phosphotyrosyl phosphatase gene (fragment
 PT for use in diagnosis of cancers; e.g. acute non-lymphocytic
 PT leukaemia)
 XX PS Claim 6: Fig 1; 73pp; English.
 XX CC A human placental cDNA library was screened with degenerate probes
 CC deduced from the partial amino acid sequence of the PTPase 1B (see
 CC AA013653 and AA013654 for probe sequences); one recombinant
 CC bacteriophage hybridised to both probes and was shown to contain a
 CC 3.2 kb fragment. The fragment was subcloned in pCM32 and sequenced
 CC The open reading frame was predicted to encode this 435 amino acid
 CC protein. The calculated mol. wt. is 49,966. PTPB is useful for
 CC treatment of ANL; myelodysplastic syndrome and myeloproliferative
 CC disorders. See also AA013644-013654.
 XX SO Sequence 435 AA;

Query Match 99.2%; Score 1336; DB 12; Length 435;

Best Local Similarity 99.2%; Pred. No. 1,76 124;
 Matches 254, Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DEPCRVAKLIPKNNKNNRYRVSPEHDSRIKIHQEDNDYINASLIMKFAQASYLTGQPL 60
 DB 29 dipcrvaklprknknrrydrvspsidhsrikihqedndyinaslkmwaaqsylltqpl 88
 QY 61 PNTGHEHEWMEWEEKSRGVMLNRYMEKGSILKAYWPFQKEEKMEFEEDNLKLTISED 120
 DB 89 pntghehewmeeweksrqvmnlrvmecksgilkaaywfpqkeekmefednlklitised 148
 QY 121 IKSYYTV--LELENTTQETREILHFHYTTPDQVPESPASFLNPLFKVRESGSLSPEN 178
 DB 149 lksyytvleleenttqetrelhfhyytwpdqvpespasflnplfkvresgslspen 208
 QY 179 GVHVCAGICRSCFPLADICILIMKKKQSSVDIKKYLIMRKPRMCLIGTAQOLR 238
 DB 209 gvvhcagiqrsctfpladrcilimkkqssvdiikkylimrkprmclicgtaqolr 268
 QY 239 YLAVIEGAKPTMGD 254
 DB 269 ylaviegaktimgd 284

RESULT 4
 AAM51206
 ID AAM51206 standard; Protein: 435 AA.

XX AC AAM51206;
 XX DT 19-DEC-2001 (first entry)
 XX DE Human PTPB Genbank Accession Number P18031
 XX KW PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
 XX KW dephosphorylation; phosphotyrosine; human; PTPB.
 XX OS Homo sapiens.
 XX FN W0200161031-A2.
 XX PD 23-AUG-2001.
 XX PF 13-FEB-2001; 2001WO-0505180.
 XX PR 14-FEB-2000; 2000US-0181769.
 XX PA (CEPT-) CEPTYR INC.
 XX PI Flint AJ, Cool DE;
 XX DR WPI: 2001-570570/64.
 XX PT Screening assays to identify agents that alter protein tyrosine
 PT phosphatase (PTP) binding to, and PTP-mediated catalytic
 PT dephosphorylation of phosphotyrosine peptide substrates
 XX PS Example 1: Page 7; 79pp; English.
 XX CC The invention relates to identifying agents which alter the interaction
 CC between a protein tyrosine phosphatase (PTP) and a tyrosine
 CC phosphorylated polypeptide using fluorescence energy signals. The methods
 CC are useful for performing screening assay to identify agents that alter
 CC PTP binding to and PTP-mediated catalytic dephosphorylation of
 CC phosphotyrosine peptide substrates. The present sequence is not given in
 CC the specification but is that of human PTPB protein sequence taken from
 CC Genbank (Accession Number: P18031). The present sequence was used to
 CC generate mutants E181A (AAM51203) and C215S (AAM51204) as described in
 CC the specification.
 CC Note: An alternative sequence for human PTPB is given in figure 1 of
 CC the specification (AAG/8262).
 XX SO Sequence 435 AA;

[illegible]

	RESULTS	5
XX	AAP058448	
XX	ID	AAP058448 standard; Protein: 415 AA.
XX	Nr	
XX	AAP058446:	
XX	25 SEP 2001 (first entry)	
XX		
XX	Human protein phosphatase 1B (PPP1B).	
XX	Homo sapiens	
XX	Protein phosphatase 1B; PPP1B; antitense; gene therapy;	
XX	tuberculosis; inflammation; tumor; prophylaxis.	
XX		
XX	Homo sapiens.	
XX	M56261640 BL.	
XX	1 JUL 2001.	
XX		
XX	IP DAN 2000: 2100075-0487-048.	
XX		
XX	IP DAN 2000: 2000075-0487-048.	
XX	(US) 1 ISIN PHARM INC.	
XX	Cowsey LM, Wyatt J.	
XX		
XX	WIT: 2001 462181/46.	
XX	D6	
XX	N ESDB: AAD1946.	
XX		
XX	New antitense compounds capable of modulating expression of human	
XX	protein phosphatase 1B useful for diagnosis, prophylaxis and treatment	
XX	of diseases associated with expression of protein phosphatase	
XX	Example 13: Column 55-60, 71pp; English.	
XX		
XX	The invention is directed to antitense compounds, particularly	
XX	oligonucleotides which are targeted to a DNA encoding protein	
XX	phosphatase 1B (PPP1B) to modulate its expression. The antitense	
XX	compounds are useful for diagnosis, prophylaxis and treatment of	
XX	diseases associated with the expression of PPP1B, to prevent or	
XX	delay infection, inflammation and tumor formation and as a	
XX	research reagent. The p11B DNA is useful in gene therapy.	
XX	The present sequence is human PPP1B protein.	
XX	Sequence 415 AA:	
XX		

Query Match	99.28	Score 1346	Id 22	Length 435
Host Local Similarity	99.28	Prod No 1.76	U21	
Matches 249	Conservative 0	Mismatches 0	Indels 2	Gaps 1
QY	1	DFPPVAKLEPPKKNPPEDVSEFTHSIRKILQIENQYINASILKMEQVRSYLLTQGL	60	
Dh	29	dfepraklplkkmrrgrdyvsgfshstrikilqgndyfnasilkmcaqsylltqgl	88	
QY	61	PNIDCHQWVWVWQKSEVVMN-NVMEKSLKSTAVWQKSEKNEPEEDPNEELITSDP	120	
Dh	89	pnidchqkwvwwqksvymnnvmeqslkstavwqsknepeepdneelittsdp	148	
QY	121	IKSYIVV--LEENNDTQETRIILHRYTWIDPQVPSSTASPLNLEPKVNSGSLSPER	178	
Dh	149	lksyivvafleednttqetrcilflfytlqdfgypssasfntlrlkrtssgslspch	208	
QY	179	GPVAVVIRSATIGSESTFETLAEETLILMOPKRNSEVSEKVVLEEMKTPMGLTQATQIR	238	
Dh	209	gpvavvirsatigsgfclaeetlilmopkrdpsedkksllcmktfnqfsgtdqftr	268	
QY	239	PSTLAIVHCAKPIIMD	254	
Dh	269	tsylavieqaklimgd	284	

C	RESULT
C	6
C	AAM51203
C	ID AAM51203 standard; Protein; 435 AA.
C	XX AC
C	XX AAM51203;
C	XX D1
C	XX 19-DEC-2001 (first entry)
C	XX DE
C	XX Human PTPIB mutant D181A.
C	XX PP:
C	XX dephosphorylation; tyrosine phosphorylated polypeptide; dephosphorylation; phosphotyrosine; human; ptpib; mutan;
C	XX OS
C	XX Homo sapiens.
C	XX SynBeltC.
C	XX Key Location/Qualifiers
C	XX FH Misc-difference /note= "Wild-type Asp substituted by Ala"
C	XX FT
C	XX W0200161041-A2.
C	XX PN
C	XX 23-AUG-2001.
C	XX PD
C	XX PF
C	XX 13-FEB-2001; 2001WO-US05180.
C	XX PR
C	XX 14-FEB-2000; 2000US 0181769.
C	XX PA
C	XX (CEPT) CEPTYR INC.
C	XX PI
C	XX Flint AJ, Cool DE;
C	XX XX
C	XX WEI; 2001-570570/64.
C	XX ER
C	XX Screening assays to identify agents that alter protein tyrosine phosphatase (ptp) binding to, and ptp-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates
C	XX Example 1, Page , 7pp, English.
C	The invention relates to identifying agents which alter the interaction between a protein tyrosine phosphatase (ptp) and a tyrosine phosphorylated polypeptide using fluorescence energy signals. The methods are useful for performing screening assay to identify agents that alter ptp binding to and ptp-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence as that of a

FT Misc-difference 251 gives a 322 residue protein"
 FT /note- "changed from Cys in wild-type to Ser in
 F-1 mutant"
 XX
 XX W09820156-A1
 XX
 XX 14-MAY-1998.
 XX
 XX 03-NOV-1997: 97MO-CA00825.
 XX
 XX 04-NOV-1996: 96US-0030408
 XX
 XX (MERI) MERCK FROST CANADA INC.
 XX
 XX Desmarais S, Ford-Hutchinson A, Friesen R, Grosset M;
 PI Kennedy H, Nicholson D, Ramchandran C, Skorey R;
 DR WPI: 1998-348103/40
 XX
 XX Enzyme binding assay for detection of useful compounds - uses mutant
 PI form of wild type enzyme, in which serine replaces cysteine at
 PT active site, to reduce interference from oxidizing/alkylating agents
 XX
 XX Disclosure: Pages 37-48; 63pp; English.
 XX
 XX The present sequence represents a mutated human PTP1B tyrosine kinase
 CC phosphatase. The protein has a truncation (comprising residues 1-320)
 CC and single point mutant (where residue 251 is changed from cysteine to
 CC serine) when compared to the wild-type PTP1B tyrosine kinase phosphatase.
 CC The invention claims for a method for use in a scintillation proximity
 CC binding assay (SPA) for proteases and phosphatases. The method involves
 CC using mutated proteases and phosphatases whereby the catalytic cysteine
 CC residue of the enzymes are replaced with a serine or alanine residue to
 CC correct the problem of interference in SPA from extraneous oxidizing and
 CC alkylating agents. The mutation affects the catalytic properties of the
 CC enzyme but does not affect their binding properties. The invention
 CC provides new ligands for use in SPA which have increased binding
 CC affinity for a tyrosine phosphatase or cysteine protease. The ligands
 CC contain at least two 4-phosphono(difluoromethyl) phenylalanine groups.
 CC which increase binding affinity of the ligand to its respective enzyme.
 CC The assay can be used to determine the ability of new ligands and
 CC compound mixtures to competitively bind with an enzyme. The method is
 CC claimed to allow a better usage of SPA in the discovery of compounds for
 CC the treatment and study of diseases, e.g. diabetes, cancer and
 CC osteoporosis.
 CC
 CC Sequence 323 AA:
 S0
 Query Match 97.6%; Score 1314.5; DB 19; Length 123;
 Best Local Similarity 97.7%; Pred. No. 1 for 122;
 Matches 253; Conservative 0; Mismatches 1; Indels 5; Gaps 2;
 QY 1 DEFGRAVAKLPRKNNENPNVPSFPHSRITKLHEDNDYINASLIKKEEPORSYLLTGPLE 60
 DB 29 dfccrvaklprknnrnyrvpsfphsrirkhgedndyinaslikkeecarsyilggpl 88
 QY 61 PNIQGHWEWVFOKSGVNLNRVMKGSIKCAQYWPQKEKEMIPEDTNLIKTLISHD 120
 DB 89 pniqghwewvfoksqgvnlrvvmkgsikcaqwpqkeekemiliednlkllisled 148
 QY 121 IKSYYIV--LLEENLTOETRELLHFRYTTWPPGCPSPASPLNLPFKVRESQSISPRH 178
 DB 149 iksyyivqlelelcttctrccllhtyctwppdrgvpspsstnltfkresasispch 208
 QY 179 GPVVVHCSAGI--GRSGTFCIATGCLLMDEKDPSSVDIKYVLLFMPKFPMDLTOTAD 235
 DB 209 gpvvvhcsagigtcrstfcicadclllmdkkrpssvdikeyllmtrkrmgltqad 268
 QY 236 QIRPSYIAVIFCAKFIQCD 254
 DB 269 qirpsyiaivcaqaklmod 287

RESULT 11
 AAM48936
 ID AAM48936 standard; protein; 323 AA.
 XX
 XX AAM48936:
 XX
 XX 26-OCT-1998 (first entry)
 XX
 XX Mutant human PTP1B tyrosine kinase phosphatase.
 XX
 XX Mutant human PTP1B tyrosine kinase phosphatase; protease; SPA;
 XX scintillation proximity binding assay; diabetes; cancer.
 XX 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.
 XX
 XX Homo sapiens.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 323
 FT /note- "The residue is encoded by CAC, but it is
 FT not specified in the specification which
 FT gives a 322 residue protein"
 FT
 FT Misc-difference 251
 FT /note- "changed from Cys in wild-type to Ser in
 FT mutant"
 XX
 XX W09820024-A1.
 XX
 XX 14-MAY-1998.
 XX
 XX 03-NOV-1997: 97MO-CA00824.
 XX
 XX 04-NOV-1996: 96US-0030411.
 XX
 XX (MERI) MERCK FROST CANADA INC.
 XX
 XX Desmarais S, Friesen R, Zamboni R;
 PI WPI: 1998-348101/30.
 DR N PSDB, AAV32607.
 XX
 XX Peptide(s) useful in binding assays for tyrosine phosphatases or
 PT cysteine proteases - contain two or more 4-phosphono(difluoromethyl)
 PT phenylalanine groups to improve binding affinity
 XX
 XX Disclosure: Pages 37-38; 59pp; English.
 XX
 XX The present sequence represents a mutated human PTP1B tyrosine kinase
 CC phosphatase. The protein has a truncation (comprising residues 1-320)
 CC and single point mutant (where residue 251 is changed from cysteine to
 CC serine) when compared to the wild-type PTP1B tyrosine kinase phosphatase.
 CC The invention provides a method for use in a scintillation proximity
 CC binding assay (SPA) for proteases and phosphatases. The method involves
 CC using mutated proteases and phosphatases whereby the catalytic cysteine
 CC residue of the enzymes are replaced with a serine or alanine residue to
 CC correct the problem of interference in SPA from extraneous oxidizing and
 CC alkylating agents. The mutation affects the catalytic properties of the
 CC enzyme but does not affect their binding properties. The invention
 CC claims for new ligands for use in SPA which have increased binding
 CC affinity for a tyrosine phosphatase or cysteine protease. The ligands
 CC contain at least two 4-phosphono(difluoromethyl) phenylalanine groups.
 CC which increase binding affinity of the ligand to its respective enzyme.
 CC The assay can be used to determine the ability of new ligands and
 CC compound mixtures to competitively bind with an enzyme. The method is
 CC claimed to allow a better usage of SPA in the discovery of compounds for
 CC the treatment and study of diseases, e.g. diabetes, cancer and
 CC osteoporosis.
 CC
 CC Sequence 323 AA:
 S0

SQ Sequence 251 AA:

Query Match 74.79; Score 1006.5; Pos 22; Length 251;

Best Local Similarity 72.48; Pred. No. 5,34,92; Mismatches 29; Indels 5; Gaps 3;

Matches 184; Conservative 37; Mismatches 29; Indels 5; Gaps 3;

QY 1 DEPCVAKIPKNNKNNPNVSPFDSRIKILHEDNDYINASLIKMEFAORSYLLTQCHL 60
 1 dphvavakipennrnyrvdsfysfthervtqnaendynaslvdcvcaqsylltqgpl 59
 Db 1 dphvavakipennrnyrvdsfysfthervtqnaendynaslvdcvcaqsylltqgpl 59

QY 61 PNTGCHFWEMWEDKSRGVNMLNRMVMEKSLKCAQYVPOKEEKNMFIHDPNKLTLTISED 120
 60 pntcghfwemwvdkrkavvmlnrvmekslkcaqyvpodkeeknmfihdpnkltltlised 118
 Db 60 pntcghfwemwvdkrkavvmlnrvmekslkcaqyvpodkeeknmfihdpnkltltlised 118

QY 121 IKSYVTELENIITTOPEFRIHFHTTWPPFSPASFLNFIKVRSGSLSPHGP 180
 121 iksyvtelelnittpofreihfhttwppfspasflnfikvrsgslsphgp 178
 Db 121 iksyvtelelnittpofreihfhttwppfspasflnfikvrsgslsphgp 178

QY 181 VVHVSAGICRSGTFCGLADTCLLLMKRKPSSVDIKKVLLEMKFRMG:IGTADQLRFS 240
 181 vvhsagicrsgtfcgladtclllmkrkpssvdikkvllmkrfrmg:igtadqlrfs 235
 Db 179 avthcsagiqrsqtlslvdclvlmekgdd--lnkqvlmmrkymglqltpdqrlfs 235

QY 241 YLAVTEGAKFIMCD 254
 241 ylavtegakfimgcd 249
 Db 236 ymallegakckimgcd 249

RESULT 14

AA859365

ID AA859365 standard; Protein; 251 AA.

AC AAB59365;

XX 21-MAR-2001 (first entry)

XX Human protein tyrosine phosphatase #2.

XX Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;

XX substrate trapping.

XX Homo sapiens.

XX MO200075139-A1

XX 14-DEC-2000.

XX 24-MAY-2000; 2000MO-UST14211.

XX 03-JUN-1999; 9908-0137319.

XX 16-JUN-1999; 9908-0334575.

XX (GOLD-) GOLD SPRING HARBOR LAB.

XX Tonks NK, Zhang S;

XX WPI: 2001-080598/09.

XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in

XX which the wild type PTP catalytic domain invariant aspartate is

XX replaced with an unphosphorylated amino acid, useful in gene therapy

XX Disclosure; Fig 1; 10pp; English.

XX The present invention provides substrate trapping mutant protein tyrosine

XX phosphatases (PTPs). They can be used to reduce the activity of tyrosine

XX phosphorylated proteins and to screen for modulators capable of altering

XX the binding of protein tyrosine phosphatases to their substrate. These

XX may be used in disease diagnosis and treatment.

Query Match 74.28; Score 999.5; Pos 22; Length 251;

Best Local Similarity 72.08; Pred. No. 2,66,91; Mismatches 29; Indels 5; Gaps 3;

Matches 183; Conservative 37; Mismatches 29; Indels 5; Gaps 3;

QY 1 DEPCVAKIPKNNKNNPNVSPFDSRIKILHEDNDYINASLIKMEFAORSYLLTQCHL 60
 1 dphvavakipennrnyrvdsfysfthervtqnaendynaslvdcvcaqsylltqgpl 59
 Db 1 dphvavakipennrnyrvdsfysfthervtqnaendynaslvdcvcaqsylltqgpl 59

QY 61 PNTGCHFWEMWEDKSRGVNMLNRMVMEKSLKCAQYVPOKEEKNMFIHDPNKLTLTISED 120
 60 pntcghfwemwvdkrkavvmlnrvmekslkcaqyvpodkeeknmfihdpnkltltlised 118
 Db 60 pntcghfwemwvdkrkavvmlnrvmekslkcaqyvpodkeeknmfihdpnkltltlised 118

QY 121 IKSYVTELENIITTOPEFRIHFHTTWPPFSPASFLNFIKVRSGSLSPHGP 180
 121 iksyvtelelnittpofreihfhttwppfspasflnfikvrsgslsphgp 178
 Db 121 iksyvtelelnittpofreihfhttwppfspasflnfikvrsgslsphgp 178

QY 181 VVHVSAGICRSGTFCGLADTCLLLMKRKPSSVDIKKVLLEMKFRMG:IGTADQLRFS 240
 181 vvhsagicrsgtfcgladtclllmkrkpssvdikkvllmkrfrmg:igtadqlrfs 235
 Db 179 avthcsagiqrsqtlslvdclvlmekgdd--lnkqvlmmrkymglqltpdqrlfs 235

QY 241 YLAVTEGAKFIMCD 254
 241 ylavtegakfimgcd 249
 Db 236 ymallegakckimgcd 249

RESULT 15

ABB66593

ID ABB66593 standard; Protein; 535 AA.

XX ABB66593;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 26571.

XX Drosophila, developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX MO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001MO-US09231.

XX 23-MAR-2000; 2000MS-191637P.

XX 11-JUN-2000; 2000US-0614150.

XX (PRK) PR CORP NY.

XX Venter JC, Adams M, Li PMD, Myers EW;

XX WPI: 2001-658860/75.

XX N-PSDB: ABL10696.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions

XX Disclosure; SEQ ID NO 26571; 21pp + Sequence listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (ABL1617b-ABL10511), expressed DNA

XX sequences (ABL1840-ABL16175) and the encoded proteins

XX (ABB5737-ABB72072).

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WPI

XX at ftp.wipo.int/pub/published_pat_sequences.

XX
Sequence 565 AA

Query Match 565 AA Score 726.57 DB 22 Length 535
 Best Local Similarity 56.6% Prod. No. 1.1e-64
 Matches 147 Conserved 42 Mismatches 56 Gaps 2

```

QY 12 NKNKRYRQSPHRRKIKHJENOVINASTLKMFLAQRSYLLDGLPNTGCHFWEMV 71
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 NQDINLYRDPYDSIVLKRISVDYINADVQLCTACQYILTQQLVDTVQHTWIMV 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 72 WDKSRGVVMNRYVWPKRSIKVAYWPKKEPKEMIFETNLTLSGDIKSYTVL 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120 WQKSRGVVMNRYVWPKRSIKVAYWPKKEPKEMIFETNLTLSGDIKSYTVL 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 129 ELENLTCTELRELIHRYITWQRCVPRSIASHINLPRVRSQSLSPHGPVWVHCSA 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 ELENLTCTELRELIHRYITWQRCVPRSIASHINLPRVRSQSLSPHGPVWVHCSA 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 189 GIGRSSTPECLADQGLIMDQSSVPRFVLEPRPFPMELIGTAQLPESTLAIVEG 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 GIGRSSTPECLADQGLIMDQSSVPRFVLEPRPFPMELIGTAQLPESTLAIVEG 296
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 248 AK 249
   |
Db 297 AK 298

```

Search completed: June 18, 2002, 14:56:48
 Job Time: 59 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 14:55:49, Search time 19.35 Seconds
(without alignments)
1267.480 Million cell updates/sec

Title: 78 09 768 626 2
Percent score: 1347
Sequence: 1 DFCGNVAKLKKNNKNNKFF ECLFESYLAVIPIAKTIMGD 254

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR71:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	99.2	435	1	tyrosine
2	1335	97.6	432	1	tyrosine
3	1290	95.8	432	1	tyrosine
4	1271	94.4	356	2	tyrosine
5	1014	75.3	363	1	tyrosine
6	1011	75.1	415	1	tyrosine
7	1010	75.0	387	1	tyrosine
8	1008	74.8	382	1	tyrosine
9	725.5	53.9	535	2	tyrosine
10	725.5	53.9	548	2	tyrosine
11	593	37.3	604	2	tyrosine
12	500	37.1	597	2	tyrosine
13	498.5	37.0	1997	1	tyrosine
14	496.5	36.9	583	2	tyrosine
15	492.5	36.6	1557	2	tyrosine
16	472.5	36.6	1432	2	tyrosine
17	485.5	36.0	1615	2	tyrosine
18	485.5	36.0	1767	2	tyrosine
19	480	35.6	377	1	tyrosine
20	474	35.2	1347	1	tyrosine
21	471.5	35.0	1262	1	tyrosine
22	471.5	35.0	1496	1	tyrosine
23	471.5	35.0	1501	2	tyrosine
24	471.5	35.0	1863	2	tyrosine
25	469.5	34.9	585	2	tyrosine
26	469.5	34.9	593	2	tyrosine
27	469.5	34.8	1301	1	tyrosine
28	468.5	34.8	593	1	tyrosine
29	467	34.7	593	1	tyrosine

30	466.5	34.6	597	1	tyrosine
31	466.5	34.6	1907	2	tyrosine
32	464.5	34.5	1445	1	tyrosine
33	463	34.4	405	2	tyrosine
34	462	34.3	1238	2	tyrosine
35	461.5	34.3	1442	1	tyrosine
36	460.5	34.2	595	1	tyrosine
37	460.5	34.1	1188	1	tyrosine
38	460	34.1	1216	2	tyrosine
39	459	34.1	405	2	tyrosine
40	459	34.1	1187	1	tyrosine
41	458.5	34.0	1422	2	tyrosine
42	457.5	34.0	595	1	tyrosine
43	457	33.9	1226	1	tyrosine
44	455.5	33.8	1897	1	tyrosine
45	454.5	33.7	1585	2	tyrosine

ALIGNMENTS

Result 1

tyrosine

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 [validated] - human

N:Altemate names: phosphotyrosine phosphatase 1b, long form, protein tyrosine phosphatase 1b, membrane bound form, pr

C:Species: Homo sapiens (man)

C:Date: 07-Apr-1994 #sequence, revision 07-Apr-1994 #rev, #date 15-Sep-2000

C:Accession: A35992; 159169; 179576; S15849; A33897; A37275

R:Chenault, J.; Schiavella, A.R.; Jost, C.A.; Erikson, R.L.; Neel, B.G.

Proc. Natl. Acad. Sci. U.S.A. 87, 2735-2739, 1990

A>Title: Cloning of a cDNA for a major human protein-tyrosine phosphatase.

A:Reference number: A35992; MUID:90207272

A:Accession: A35992

A:Molecule type: mRNA

A:Residues: 1-435 cDNA

A:Cross references: GB M31724, NID:9190741, EFIN AAA6023 1; PID:9190742

P:Brown, Shiner, S.; Johnson, K.A.; Lawrence, T.R.; Johnson, C.; Bruskien, A.; Green, N

Proc. Natl. Acad. Sci. U.S.A. 87, 5148-5152, 1990

A>Title: Molecular cloning and chromosome mapping of the human gene encoding protein

A:Reference number: 159169; MUID:90311360

A:Accession: 159169

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 165-435 cDNA

A:Cross references: GB M31684, NID:9190777; EFIN AAA60158 1; PID:9190779

R:Palmer, C.J.; Loh, D.S.V.; Chiba, H.; Hovet, T.; Tong, P.H.

Biochem. J. 276, 315-323, 1991

A>Title: Purification and characterization of a higher-molecular-mass form of protein

A:Reference number: S15849; MUID:91264781

A:Accession: S15849

A:Molecule type: protein

A:Residues: 1-321 cDNA

R:Barford, D.; Flint, A.J.; Tonks, N.K.

submitted to the Brookhaven Protein Data Bank, September 1994

A:Reference number: A52879; PID:200P

A:Content: annotation, X-ray crystallography, 2.8 angstroms, residues 5-282

Barford, D.; Flint, A.J.; Tonks, N.K.

Science 263, 1397-1404, 1994

A>Title: Crystal structure of human protein tyrosine phosphatase 1B.

A:Reference number: A38904; MUID:94174273

A:Cross-references: GB:140595; NID:q755042; P1DN:AAA64615.1; P1D:q755043
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:40-266/Domain: protein-tyrosine-phosphatase homology cpps
 F:215/Active site: Cys (phosphotyrosine intermediate) *status predicted
 F:221/Binding site: substrate phosphate (Arg) *status predicted

Query Match 95.8% Score 1290; DB 1; Length 432;
 Host Local Similarity 94.5%; Pred. No. 10-97; Indels 2; Gaps 1;
 Matches 242; Conservative 5; Mismatches 3

DB 1 DEPCVAKLPKKNRRYDVSPDHSRIKIQEDNDYINASTIMEEDQNSYITQGPL 60
 |||||
 DB 29 DPCVAKLPKKNRRYDVSPDHSRIKIQEDNDYINASTIMEEDQNSYITQGPL 88
 |||||
 DB 41 PNTCGHEWMEWQSKRGVVMNRYMEKSLKCAQYVMEKEKEMIFETN:KLTITSED 120
 |||||
 DB 89 PNTCGHEWMEWQSKRGVVMNRYMEKSLKCAQYVMEKEKEMIFETDGLKLTISED 148
 |||||
 DB 121 IKSYIV--LEFNITQTRRLHPHTTMDPGVPSPASHLPKVRSGSLSPRH 178
 |||||
 DB 149 VKSYYIVQLEENITKREILHPHTTMDPGVPSPASHLPKVRSGSLSPRH 208
 |||||
 DB 179 GPVVMHSAITGSGTFTLATITLLMKRKPSSVYIKVLEMPKFMGLTQTADQLR 238
 |||||
 DB 209 GPVVMHSAITGSGTFTLATITLLMKRKPSSVYIKVLEMPKFMGLTQTADQLR 268
 |||||
 DB 239 FSYLAVIEAKFTMGD 254
 |||||
 DB 269 FSYLAVIEAKFTMGD 284
 |||||

RESULT - 4
 JMW0049
 protein-tyrosine-phosphatase (EC 3.1.3.48) 1 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 03-Dec-1999
 C:Accession: JMW0049

R:Jung, R.J.; Kang, Y.S.; Kim, C.W.
 Histochem. Histochem. Res. Commun. 246, 239-242, 1998
 A:Title: Multiple phosphorylation of chicken protein tyrosine phosphatase 1 and human p1
 A:Reference number: JMW0049; MIMD:98262948
 A:Accession: JMW0049
 A:Molecule type: mRNA
 A:Residues: 1-356 <MIMD>
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase
 C:Keywords: phosphoric monoester hydrolase
 F:27/Domain: protein-tyrosine-phosphatase homology cpps

Query Match 94.4% Score 1271; DB 2; Length 356;
 Host Local Similarity 93.4%; Pred. No. 2-80-96; Indels 2; Gaps 1;
 Matches 239; Conservative 10; Mismatches 5

DB 1 DEPCVAKLPKKNRRYDVSPDHSRIKIQEDNDYINASTIMEEDQNSYITQGPL 60
 |||||
 DB 16 DPCVAKLPKKNRRYDVSPDHSRIKIQEDNDYINASTIMEEDQNSYITQGPL 75
 |||||
 DB 61 PNTCGHEWMEWQSKRGVVMNRYMEKSLKCAQYVMEKEKEMIFETN:KLTITSED 120
 |||||
 DB 76 PNTCGHEWMEWQSKRGVVMNRYMEKSLKCAQYVMEKEKEMIFETDGLKLTISED 135
 |||||
 DB 121 IKSYIV--LEFNITQTRRLHPHTTMDPGVPSPASHLPKVRSGSLSPRH 178
 |||||
 DB 146 IKSYIVRLLENDLTETREILHPHTTMDPGVPSPASHLPKVRSGSLSPRH 195
 |||||
 DB 179 GPVVMHSAITGSGTFTLATITLLMKRKPSSVYIKVLEMPKFMGLTQTADQLR 238
 |||||
 DB 196 GPVVMHSAITGSGTFTLATITLLMKRKPSSVYIKVLEMPKFMGLTQTADQLR 255
 |||||
 DB 239 FSYLAVIEAKFTMGD 254
 |||||

DB 256 FSYLAVIEAKFTMGD 271

RESULT 5
 S14294
 protein-tyrosine-phosphatase (EC 3.1.3.48) 11A rat

C:Species: Rattus norvegicus (Norway Rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S14294; S21831
 R:Swartup, G.; Kamakur, S.; Kadha, V.; Kema, V.
 PNAS Lett. 280, 65-69, 1991
 A:Title: Molecular cloning and expression of a protein-tyrosine phosphatase showing h
 A:Reference number: S14294; MIMD:31184422
 A:Accession: S14294
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-363 <SWA2>
 A:Cross-references: GB:X58828; NID:q56095; P1DN:AAA1633.1; P1D:q56096
 R:Swartup, G.; Kamakur, S.; Kadha, V.; Kema, V.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S21831
 A:Accession: S21831
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-363 <SWA2>
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase
 C:Keywords: alternative splicing; DNA binding; phosphoprotein; phosphoric monoester h
 F:42-264/Domain: protein tyrosine phosphatase homology cpps
 F:216/Active site: Cys (phosphotyrosine intermediate) *status predicted
 F:222/Binding site: substrate phosphate (Arg) *status predicted

Query Match 75.3% Score 1014; DB 1; Length 363;
 Host Local Similarity 71.9%; Pred. No. 2-80-75; Indels 6; Gaps 3;
 Matches 184; Conservative 38; Mismatches 28

DB 1 DEPCVAKLPKKNRRYDVSPDHSRIKIQEDNDYINASTIMEEDQNSYITQGPL 60
 |||||
 DB 31 DPCVAKLPKKNRRYDVSPDHSRIKIQEDNDYINASTIMEEDQNSYITQGPL 90
 |||||
 DB 61 PNTCGHEWMEWQSKRGVVMNRYMEKSLKCAQYVMEKEKEMIFETDGLKLTISED 120
 |||||
 DB 91 PNTCGHEWMEWQSKRGVVMNRYMEKSLKCAQYVMEKEKEMIFETDGLKLTISED 149
 |||||
 DB 121 IKSYIV--LEFNITQTRRLHPHTTMDPGVPSPASHLPKVRSGSLSPRH 178
 |||||
 DB 150 VKSYYIVQLEENITKREILHPHTTMDPGVPSPASHLPKVRSGSLSPRH 209
 |||||
 DB 179 GPVVMHSAITGSGTFTLATITLLMKRKPSSVYIKVLEMPKFMGLTQTADQLR 238
 |||||
 DB 210 GPVVMHSAITGSGTFTLATITLLMKRKPSSVYIKVLEMPKFMGLTQTADQLR 266
 |||||
 DB 239 FSYLAVIEAKFTMGD 254
 |||||
 DB 267 FSYLAVIEAKFTMGD 282
 |||||

RESULT 6
 A33899
 protein-tyrosine-phosphatase (EC 3.1.3.48) 1 - human
 N:Alternate names: protein-tyrosine-phosphatase, T-cell specific
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1990 #sequence_revision 02-May-1994 #text_change 07-May-1999
 C:Accession: A33899; C60145; A45142
 R:Cooper, D.E.; Tonks, N.K.; Charbonneau, B.; Walsh, K.A.; Fischer, E.H.; Krebs, E.G.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5257-5261, 1989
 A:Title: cDNA isolated from a human T cell library encodes a member of the protein-ty
 A:Reference number: A33899; MIMD:89315776
 A:Accession: A33899
 A:Molecule type: mRNA
 A:Residues: 1-415 <COO>
 A:Cross-references: GB:M25393

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 14:55:50 : Search time 11.04 Seconds
(Without alignments)
890 R30 Million cell updates/sec

Title: US-09-788-626-2
Perfect score: 1347
Sequence: 1 DFKCVRVAKIPKKNKNNKPPVND : DOLKPSYLAIVHCAKPIKMGD 254

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	99.2	435	1 P7N1_HUMAN	P18031 homo sapien
2	1315	97.6	432	1 P7N1_RAT	P20417 rattus norv
3	1299	96.4	432	1 P7N1_MOUSE	P35821 mus musculu
4	1278	94.9	434	1 P7N1_CHICK	O13016 gallus gall
5	1014	75.3	463	1 P7N2_RAT	P35233 rattus norv
6	1011	75.1	435	1 P7N2_HUMAN	P17706 homo sapien
7	1008	74.8	382	1 P7N2_MOUSE	O06180 mus musculu
8	498.5	37.0	1997	1 P7P1_HUMAN	P23467 homo sapien
9	492.5	36.6	1630	1 P7P1_DROME	P35952 drosophila
10	480	35.6	377	1 P7P2_DICDI	P34138 dictyostell
11	474	35.2	1337	1 P7P1_HUMAN	P35235 mus musculu
12	469.5	34.9	585	1 P7P9_DROME	P35832 drosophila
13	469	34.8	1301	1 P7P9_MOUSE	O06124 homo sapien
14	468.5	34.8	593	1 P7N8_HUMAN	P43378 homo sapien
15	467	34.7	593	1 P7N9_HUMAN	P41499 homo sapien
16	465.5	34.6	593	1 P7N8_MOUSE	P23470 mus musculu
17	464.5	34.5	1445	1 P7P6_HUMAN	O64455 mus musculu
18	462	34.3	1238	1 P7P1_MOUSE	O05909 mus musculu
19	461.5	34.3	1442	1 P7P6_MOUSE	O08948 gallus gall
20	458.5	34.0	1122	1 P7N6_CHICK	P29333 mus musculu
21	457.5	34.0	595	1 P7N6_MOUSE	P10586 homo sapien
22	455.5	33.8	1897	1 P7P3_HUMAN	P26045 homo sapien
23	452	33.6	913	1 P7N3_HUMAN	P29350 homo sapien
24	447.5	33.2	595	1 P7N6_HUMAN	P29074 homo sapien
25	441.5	32.8	926	1 P7P4_HUMAN	P28827 homo sapien
26	441	32.7	1452	1 P7P4_MOUSE	P28828 mus musculu
27	441	32.7	1452	1 P7P4_MOUSE	P23468 homo sapien
28	440.5	32.7	1912	1 P7P4_HUMAN	P18433 homo sapien
29	437.5	32.5	802	1 P7P4_HUMAN	Q12923 homo sapien
30	435.5	32.3	2485	1 P7P4_HUMAN	Q03348 rattus norv
31	434.5	32.3	796	1 P7P4_FAT	P23352 mus musculu
32	430	31.6	802	1 P7N8_MOUSE	P23469 homo sapien
33	429	31.8	700	1 P7P6_HUMAN	

34	427	31.7	699	1 P7P6_MOUSE	P49446 mus musculu
35	423	31.4	1439	1 P7P6_HUMAN	O15262 homo sapien
36	420	31.2	780	1 P7N1_HUMAN	O05209 homo sapien
37	420	31.2	979	1 P7P6_MOUSE	O06673 mus musculu
38	420	31.2	1304	1 CD45_HUMAN	P08575 homo sapien
39	418.5	31.1	2314	1 P7P2_HUMAN	P23471 homo sapien
40	418	31.0	1152	1 CD45_MOUSE	P06800 mus musculu
41	416.5	30.9	2029	1 LAR_DROME	P16621 drosophila
42	416	30.9	775	1 P7N6_MOUSE	P35831 mus musculu
43	416	30.9	1001	1 P7P6_MOUSE	P80560 mus musculu
44	416	30.9	1004	1 P7P6_RAT	O63475 rattus norv
45	416	30.9	1457	1 P7P6_MOUSE	P35822 mus musculu

ALIGNMENTS

Result ID	1	PTN1_HUMAN	STANDARD	PTN1	435 AA
AC	P18031	US0904: US0904			
DT	01-NOV-1990	(Rel. 16, Created)			
DT	01-NOV-1990	(Rel. 16, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, last annotation update)			
DE	protein-tyrosine phosphatase, non receptor type 1 (PC 3.1.3.48)				
DE	(protein-tyrosine phosphatase 1b) (PTP-1b).				
GN	PTP1B OR PTP1B.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N A				
RC	TISSUE=Placenta;				
EX	MEDLINE=36207/2; PubMed=215721.				
KA	Chernoff J., Schievella A.R., Jost C.A., Erikson R.L., Neel B.G.;				
KA	Cloning of a cDNA for a major human protein-tyrosine phosphatase.;				
RI	Proc. Natl. Acad. Sci. U.S.A. 87:2735-2739(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
EX	MEDLINE=36211/2; PubMed=215424;				
KA	Brown-Shimmer S., Johnson K.A., Lawrence J.B., Johnson C.,				
KA	Bruskin A., Green N.R., Hill D.E.;				
KA	Beasley O.F., Bird C.P., Blakey S.F., Bridgman A.N., Brown A.J.,				
RT	Molecular cloning and chromosome mapping of the human gene encoding				
RT	protein phosphotyrosyl phosphatase 1b.;				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:5148-5152(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
KA	Donoukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,				
KA	Jones M., Slavides G., Almeida J.P., Barbae A.K., Baguley C.L.,				
KA	Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,				
KA	Huckley E., Hunt A.K., Hunt S.E., Jakusch K., Johnson C.M., Johnson D.,				
KA	Huck D., Hurtt W., Hunter A.P., Carder C., Carter N.P.,				
KA	Chapman J.C., Clapp M., Clark C., Clark L.N., Clark S.Y., Clee G.M.,				
KA	Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.P.,				
KA	Coulson A., Corliffe G.J., Deaman R., Dhami P., Dunn M.,				
KA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,				
KA	Graham D.V., Griffiths C., Griffiths M.N.D., Galliani R., Hall R.E.,				
KA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,				
KA	Huckle E., Hunt A.K., Hunt S.E., Jakusch K., Johnson C.M., Johnson D.,				
KA	Key M.P., Kimberley A.M., King A., Knights K., Lloyd G.K., Lawlor S.,				
KA	Lavoslavskii M.H., Leverisa M., Lloyd C., Lloyd D.M., Lovell J.D.,				
KA	Marsh V.L., Martin S.L., McNamara L.J., Mclay K., McMurray A.A.,				
KA	Maline S., Mistry D., Moore M.T., Mullikin J.C., Nickerson T.,				
KA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,				
KA	Phillimore H.J.C.T., Prachinangam S.R., Plumb K.W., Ramsay H.,				
KA	Rice C.M., Ross M.P., Scott C.E., Sehra H.K., Showkdeen R., Sims S.,				
KA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Stinson J.E.,				
KA	Swann M., Symantre N., Taylor F., Tee L., Thomas D.W., Thorpe A.,				
KA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,				
KA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,				
KA	Wimling L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Brock S.,				

ID PNTL_MOUSE STANDARD: PRT: 432 AA.
 AC P20417;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 1 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase 1b) (PTP-1b).
 GN PTPN1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
 OC NCHI_taxid=10116;
 OX NCHI_taxid=10116;
 RN 111
 RP SEQUENCE FROM N.A.
 RC MEDLINE-90160454; PubMed-2154749;
 RA Guan K., Han R.S., Watson S.J., Geahlen R.L., Dixon J.F.;
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1501-1505(1990).
 CC Cloning and expression of a protein-tyrosine-phosphatase.*
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED TO THE ENDOPLASMIC RETICULUM VIA
 CC ITS C-TERMINAL DOMAIN WITH ITS PHOSPHATASE DOMAIN ORIENTED TOWARDS
 CC THE CYTOSOL.
 CC -1- TISSUE SPECIFICITY: FOUND IN SEVERAL TISSUES INCLUDING CENTRAL
 CC NERVOUS SYSTEM, LIVER AND KIDNEY. A HIGH LEVEL OF EXPRESSION WAS
 CC FOUND IN THE HIPPOCAMPI.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
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 CC -----
 CC EMRL: M31962; AAC79516.1; -
 CC PIR: A14845; A14845.
 CC HSSP: P18041; 1PTX.
 CC InterPro: IPR000340; DS-phosphatase.
 CC InterPro: IPR003874; TYR-phosphatase.
 CC InterPro: IPR006242; TYR_prot_phphatase.
 CC Pfam: PF00102; X-phosphatase.1.
 CC PRINTS: PR00700; PRTYPHPTASE.
 CC SMART: SM00194; PTPC.1.
 CC SMART: SM00012; PTPC_DSPC.1.
 CC SMART: PS00383; TYR_PHOSPHATASE_1.
 CC PROSITE: PS50056; TYR_PHOSPHATASE_2.1.
 CC PROSITE: PS50055; TYR_PHOSPHATASE_PTP.1.
 CC K1 Hydrolyase.
 CC ET DMAPIN 43 288 PROTEIN-TYROSINE PHOSPHATASE.
 CC ACT_SITE 215 215 BY SIMILARITY.
 CC SQ SHOENCE 432 AA 40074 MW: 106450aa18rcr1 CR644;
 QY Query Match 97.64; Score 13.5; DB 1; Length 432;
 DB Best Local Similarity 95.78; Pred. No. 1,2e-110;
 DB Matches 245; Conservative 7; Mismatches 2; Indels 2; Gaps 1;
 QY 1 DPGHVAALPKNNKNNRYDVSYPDHSKIKLHQRNRYINASLIKMEFAOSYLLTGGPI. 60
 DB 29 DPGHVAALPKNNKNNRYDVSYPDHSKIKLHQRNRYINASLIKMEFAOSYLLTGGPI. 88
 QY 61 PNTGCHHEMWEOKSKGVMLINKVMKGSKCAQYWFQKEKIMTETTR:KLTG:SEED 120
 DB 89 PNTGCHHEMWEOKSKGVMLINKVMKGSKCAQYWFQKEKIMTETTR:KLTG:SEED 148
 QY 121 TRSYTYV--LELENTLTQETREILHFTTTWDFGVPSPASFLNFKVWESGSLSEEH 178
 DB 149 VASVYTHVQIILENLATQFARELIHPHYTWDFGVPSPASFLNFKVWESGSLSEEH 208

QY 179 GPVWVCASACIGSCHECIADTCLLLMKRKDDSYD:KKVL:EMKFFMGL:IGTADQLR 238
 DB 209 GPVWVCASACIGSCHECIADTCLLLMKRKDDSYD:KKVL:EMKFFMGL:IGTADQLR 268
 QY 239 FSVLAIVEGAKFTMGD 254
 DB 269 FSVLAIVEGAKFTMGD 284
 RESULT 3
 PNTL_MOUSE STANDARD: PRT: 432 AA.
 AC P35821; O62131; O60840; O64498; O99JST;
 ID 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 1 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase 1b) (PTP-1b) (Protein-tyrosine
 DE phosphatase HA2) (PTP-HA2).
 GN PTPN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OC NCHI_taxid=10090;
 OX NCHI_taxid=10090;
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RA MEDLINE-92328784; PubMed-1378268;
 RA Miyasaka H., Li S.S.L.;
 RT "The cDNA cloning, nucleotide sequence and expression of an
 RT intracellular protein tyrosine phosphatase from mouse testis.*"
 RT Biochem. Biophys. Res. Commun. 185:818-825(1992).
 RN 121
 RP SEQUENCE FROM N.A.
 RA Liao K., Lane M.D.;
 RT Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN 131
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RA Park K., Byun S.;
 RT Submitted (MAY 1996) to the EMBL/GenBank/DBJ databases.
 RN 141
 RP SEQUENCE OF 102-213 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RA MEDLINE-9513432; PubMed-7832766;
 RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
 RT "A novel receptor-type protein tyrosine phosphatase with a single
 RT catalytic domain is specifically expressed in mouse brain.*"
 RT Biochem. J. 305:499-504(1995).
 RN 151
 RP SEQUENCE OF 161-432 FROM N.A.
 RA Strausberg R.;
 RT Submitted (APR 2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED TO THE ENDOPLASMIC RETICULUM VIA
 CC ITS C-TERMINAL DOMAIN WITH ITS PHOSPHATASE DOMAIN ORIENTED TOWARDS
 CC THE CYTOSOL (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN TESTIS. ALSO FOUND IN KIDNEY,
 CC SPLEEN, MUSCLE, LIVER, HEART AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMRL: M97590; -; NOT ANNOTATED_CDS.
 CC EMBL: L40595; AAA64615.1; -

F1	FARMO HYD	4.78	4.78	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	4.42	4.42	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	4.41	4.41	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	4.76	4.76	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	4.91	4.91	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	4.96	4.96	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	4.4	4.4	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	4.41	4.41	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	5.01	5.01	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	5.25	5.25	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	5.36	5.36	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	5.02	5.02	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	6.03	6.03	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	6.18	6.18	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	6.28	6.28	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	6.7	6.67	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	6.66	6.66	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	6.9	6.9	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	7.1	7.1	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	7.72	7.72	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	7.84	7.84	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	7.90	7.90	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	8.24	8.24	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	9.10	9.1	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	9.47	9.47	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	26.1	26.1	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	9.18	9.2	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO HYD	13.47	13.47	N LINKED (GLC'NAc' - -)	(POTENTIAL)

[illegible]

RT "SH2-containing phosphotyrosine phosphatase as a target of protein
 RT tyrosine kinases.";
 RL Science 259:1607-1611(1993).
 RN 121
 RA X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS) OF 4-103,
 RX MEDLINE 94363243; PubMed-752135;
 RA Lee C.-H., Komlos D., Jacques S., Margolis B., Schleissner J.,
 RA Sheelson S.E., Kurlyan J.,
 RL "Crystal structures of peptide complexes of the amino-terminal SH2
 RL domain of the SHP tyrosine phosphatase.";
 RL Structure 2:423-436(1994).
 CC -1- FUNCTION: THIS PTASE ACTIVITY MAY DIRECTLY LINK GROWTH FACTOR
 CC RECEPTORS AND OTHER SIGNALING PROTEINS THROUGH PROTEIN TYROSINE
 CC PHOSPHORYLATION. THE SH2 REGIONS MAY INTERACT WITH OTHER CELLULAR
 CC COMPONENTS TO MODULATE ITS OWN PHOSPHATASE ACTIVITY AGAINST
 CC INTERACTING SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2)O -> protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: PHOSPHORYLATED BY TYROSINE-PROTEIN KINASES.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. SUBCLASS THAT CONTAINS SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -----
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 CC -----
 CC EMBL: A04663; ; NOT_ANNOTATED_CDS.
 CC PIR: A46209; A46209.
 DR PDB: 1AY6; 3I-AUG-94.
 DR PDB: 1AY6; 3I-AUG-94.
 DR PDB: 1AYC; 3I-AUG-94.
 DR PDB: 1AYD; 3I-AUG-94.
 DR MCD: MCI:99511; ptptn1.
 DR InterPro: IPR0009480; SH2.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; TYR_prot_phphatase.
 DR Pfam: PF00012; Y_phosphatase; 2.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRYPPHPTASE.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR SMART: SM00194; ptpcr; 1.
 DR SMART: SM00352; SH2; 2.
 DR PROSITE: PS00393; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00566; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00555; TYR_PHOSPHATASE_PTP; 1.
 DR PROSITE: PS50011; SH2; 2.
 KW Hydrolyase; SH2 domain; Repeat; Phosphorylation; 3D-structure.
 FT DOMAIN 6 102
 FT DOMAIN 112 216 SH2 1.
 FT DOMAIN 276 521 SH2 2.
 FT ACT_SITE 463 463 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 463 463 HY_SIMILARITY.
 SC SOURCE: 585 AA; 66816 MW; 663554f929d8f72a CRC64.

Query Match	34.9%	Score 469.5	Dh 1	Length 588
Best Local Similarity	37.8%	Prod. No. 1.5e 34		
Matches	96	Conservative	50	Mismatches 85
			Indels	23
			Gaps	4
QY	11	KNKNRYRQVSPFHSKILHDP	-----NINYNASLILKM	-----FAQRSTYLLIQ
Db	272	ENKNKRPKNLIPGUTVVLLHSP	PPRPVSVYINANILMPETK	INNSKRSKSYLATQ
QY	58	GDPLNTCHFWEMWQKSPQVVM	INPVEKSGKAGAYQYKREK	FTPLNKLTLI
Db	332	QGLQNTFVDPKRWYQFNSPV	YMTKRVYQKRSKSYWPD	-----DEYALKEGVMPVENV
QY	118	SEDIKSYVLELE	-----NLITQETREILH	PHYTWDPGVESVAFINLFKVE

```

Db 389 KESAHADTLEBELSKYSQALLQINTERVWQYHFRWPHGVSDDSGVLDLEFVHH 448
QY 171 SOSLSHPCHPVAVHCSAGIGRSCGCIAMICLGLMKKMDKSVCLIKKVLIMRKRFMC: 230
Db 449 KOESTVDMSPVAVHCSAGIGRSCGCIAMICLGLMKKMDKSVCLIKKVLIMRKRFMC: 508
QY 231 IOTADQLEFSTYLAIV 244
Db 509 VQTMQVRYRYMAV 522

RESULT 13
PTP9_DROME STANDARD: FRI, 1301 AA.
ID PTP9_DROME 35832:
AC 01-JUN-1994 (rel. 29, Created)
DT 01-JUN-1994 (rel. 41, Last sequence update)
DE 01-MAR-2002 (rel. 41, Last annotation update)
DE Protein-Tyrosine phosphatase 99A precursor (EC 3.1.3.48) (Receptor-linked protein-tyrosine phosphatase 99A).
GN PTP99A.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Phlebotomidae; Neoptera; Endopterygota; Lepidoptera; Brachyoptera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11
RP SOURCE FROM N.A.
RC TISSUE-Eye imaginal disk;
RX MEDLINE=92107940; PubMed=1662390;
RA Haribaran I.K., Chuang P.-I., Rubin G.M.;
RT Cloning and characterization of a receptor class phosphotyrosine phosphatase gene expressed on central nervous system axons in Drosophila melanogaster.
RT Proc Natl Acad Sci U S A 88:11266-11270(1991).
RL 13
RN 12
RP SOURCE FROM N.A.
RC TISSUE-embryo;
RX MEDLINE=92034985; PubMed=1657402;
RA Tian S.-S., Tsoulfas P., Zinn K.;
RT Three receptor-linked protein tyrosine phosphatases are selectively expressed on central nervous system axons in the Drosophila embryo.
RT Cell 67:675-685(1991).
RN 13
RP SOURCE FROM N.A.
RC TISSUE-embryo;
RX MEDLINE=92034985; PubMed=1657402;
RA Yang X., Snow K.T., Bahri S.M., Oon S.H., Chia W.;
RT Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a subset of developing axons and pioneer neurons in the embryonic CNS.
RT Cell 67:661-671(1991).
CC -1- FUNCTION: MAY PLAY A KEY ROLE IN SIGNAL TRANSDUCTION AND GROWTH CONTROL.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O -> protein tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS THAT DIFFER IN THEIR C-TERMINAL TAILS ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN TYROSINE PHOSPHATASE DOMAINS.
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CC

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DR EMBL: M81795; AAA28483.1; -
DR EMBL: M80359; AAA28485.1; -
DR EMBL: M80464; AAA28486.1; -
DR PIR: A41622; A41622
DR PIR: A41214; A41214
DR PIR: B41214; B41214
DR PIR: B41215; B41215
DR HSSP: P18052; 1YFO.
DR P1Phas; P8m0004369; PTP99A.
DR InterPro: IPK003361; FN_111.
DR InterPro: IPK003362; FN111_repeat.
DR InterPro: IPP000187; TYR_phosphatase.
DR InterPro: IPP000242; Tyr_prol_phphatase.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00102; Y-phosphatase; 2.
DR PRINTS: PR00014; FNTYPT11.
DR PRINTS: PR00700; PRTPHPTASE.
DR SMART: SM00060; FN3; 2.
DR SMART: SM0194; PTP; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00555; TYR_PHOSPHATASE_2; 1.
DR Transmembrane; Hydrophase; Repeat; Signal; Alternative splicing.
KW SIGNAL
FT CHAIN 1 301
FT DOMAIN 30 392
FT TRANSMEM 393 416
FT DOMAIN 417 1301
FT DOMAIN 64 108
FT DOMAIN 169 268
FT DOMAIN 269 368
FT DOMAIN 497 747
FT DOMAIN 748 975
FT ACT_SITE 682 682
FT DOMAIN 1076 1091
FT CARBOHYD 33 33
FT CARBOHYD 176 176
FT CARBOHYD 212 212
FT CARBOHYD 278 278
FT CARBOHYD 322 322
FT CARBOHYD 336 336
FT VARSPIC 1050 1119
FT CONFLICT 586 586
FT CONFLICT 1205 1205
SQ SOURCE 1301 AA; 145336 MW; 824153194ACAS5b) CRC64:

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Query Match 34 88; Score 469; DB 1; Length 1301;
Best Local Similarity 37.78; Pred. No. 4,76-34; Indels 24; Gaps 8;
Matches 96; conservative 61; Mismatches 77;
QY 1 DEPCVANKIPKNNKRRHYDVSPPDHSKIKH---QEDN-DY NASLAKMHAORSYIL 55
Db 491 DLPCDSHPENKRNKRYLNTLAYDHSVHLIPKGRKNNLYINANFIDYKSHAFIG 550
QY 56 TQGLPRTCCIDHEWYMKSKSGVAVLNPWEKSGSLKFAQWPAQCEKEEMFEDTNKLT 115
Db 551 TQGLPRTDPCDHWMTIMQVVALIMVILNLYVGRPKCLMMP-----KQGVETVGVIC 606
QY 116 LISEDIKSYTV--LELENLTQETRE-----LIHFVTVWDFGVSPASTFLNFK 167
Db 607 LIEEVMSTYVTRKTLQIKLKLRKKCKTEKLVQYVHTNMPDKGTDPHPLVNF-- 663
QY 168 VPPSSNSV--PQGVAVVHCSAGIGRSCGCIAMICLGLMKKMDKSVCLIKKVLIMRKRF 226
Db 664 VKRSSANFVEMGPIVAVMSAGV--PTGTYIVLDMFKQYCK--NIVNVPFLRITPAO 720
QY 227 RMLIOTADCLEFSTYLAIV 246
Db 721 RMLVQTMQVRYRYMAV 740

RESULT 14

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100 HUMAN
 101 P100 HUMAN
 102 STAMINAD
 103 PRL
 104 593 AA
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CC TISSUE SPECIFICITY: WIDELY EXPRESSED IN HUMAN TISSUES;
 CC PARTICULARLY ABUNDANT IN HEART, BRAIN, AND SKELETAL MUSCLE.
 CC -1- PTM: PHOSPHORYLATION OF TYR RESIDUES AT THE C-TERMINUS BY
 CC PLATELET-DERIVED GROWTH FACTOR CREATES A BINDING SITE FOR THE SH2
 CC DOMAIN OF GRB2.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. SUBCLASS THAT CONTAINS SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
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 CC or send an email to license@sb.sib.ch).
 CC
 CC EMBL: 108807; -1- NOT_ANNOTATED_CDS.
 CC EMBL: X70766; CAA50045.1; -1-
 CC EMBL: D13540; HAA02740.2; -1-
 CC EMBL: L07527; AAL17022.1; -1-
 CC EMBL: L03535; AAL16611.1; -1-
 CC PIR: J08055; J08055.
 CC PDB: 2SH2; 16-FEB-99.
 CC MIM: 176876; -1-
 CC InterPro: IPR000980; SH2.
 CC InterPro: IPR00387; TYR_phosphatase.
 CC InterPro: IPR00242; Tyr_Proc_phosphatase.
 CC Pfam: pf00102; SH2; 2.
 CC Pfam: pf00102; Y_phosphatase; 1.
 CC PRINTS: PR00700; PREYPHPTASE.
 CC PRINTS: PR00401; SH2DOMAIN.
 CC SMART: SM00194; PTFC; 1.
 CC SMART: SM00252; SH2; 2.
 CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS00356; TYR_PHOSPHATASE_2; 1.
 CC PROSITE: PS00355; TYR_PHOSPHATASE_PTP; 1.
 CC PROSITE: PS00011; SH2; 2.
 CC K1 Hydroxylase: SH2 domain; Repeat: Phosphorylation; 3D structure.
 CC FT DOMAIN 6 102 SH2 1.
 CC FT DOMAIN 112 216 SH2 2.
 CC FT DOMAIN 276 517 PROTEIN-TYROSINE PHOSPHATASE.
 CC ACT_SITE 459 459
 CC MOD_RES 542 542 PHOSPHORYLATION (BY PDGFR).
 CC MOD_RES 580 580 PHOSPHORYLATION (BY PDGFR).
 CC FT CONFLICT 535 535 S > R (IN REF. 3).
 CC FT CONFLICT 548 548 S > P (IN REF. 4).
 CC SOURCE 593 AA; 68011 MW; 90DHFFVAF56GCH45 CRC64;
 Query Match 34.88; Score 468.5; DB 1; Length 593;
 Best Local Similarity 48.08; Pred. No. 1,9e+14;
 Matches 95; Conservative 51; Mismatches 85; Indels 19; Gaps 4;
 11 KNNRRNRVSPDPDRIRKIHQD-----NDYINASLKKM-----FAQSYLLIG 57
 272 ENKKNRKNLLEPLDKRYVLLGCFNELFVSQYANALIMLEELKNSKPNASTATIG 341
 58 GPLPNTGHEFWMEQSKGVVALNFMKSGSLKQVYFQKEKEMIPEDNLEKTLI 117
 332 CTGNIIVNGWVWVFGNSVYVWIKVIRKSGSYVWV-----TVAALNTVYMKPKV 388
 118 SEDIKSYIVLELENTLQ-----TRELHHTYTPDPGFVSPASTNLFKYRESGSL 174
 389 KESAAIDYTLRELKRSKVQGNTEFTWYHFTWPDHGVSPGVALDELEVHKEQES 448
 175 SPEGPIPVVNCAGTGSQIFCLADPGLIMDKKPKDSSNLIKVLIMKKPFWGGLIOTA 234
 449 IMDGPIVVCASGIGRTGFTVIDLIDILIREGVCDIDIVKTIQWVRSQSGWQTE 508
 235 DQLESYLAV 244
 509 AQYRPIYMAV 518

• •

GenCOPA version 4.5
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OM protein - protein search, using sw model

Run on: Tue Jun 18, 2002, 14:55:50 : Search time 26.51 seconds
(without alignments)
1657.515 Million cell updates/sec

Title: US-09-788-626-2
Perfect score: 1347
Sequence: 1 DFCPRVAKLPRKNRPNRYRN DQIRFSYLAIVESAKFMID 254

Scoring table: HUSUM62
Gapop 10.0 , Gapext 0.5

Searchd: 562222 seqs, 12294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

SPREML15:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_ornathel:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeophag:

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1336	99.2	414	4	Q9N004	Q9N004 homo sapien
2	1166	86.6	433	13	Q9P191	Q9P191 brachydanio
3	1011	75.1	353	4	Q96AN5	Q96AN5 homo sapien
4	1011	75.1	387	4	Q96H27	Q96H27 homo sapien
5	1008	74.8	406	11	Q922E7	Q922E7 mus musculu
6	739	54.9	322	13	Q91H44	Q91H44 putamotrygo
7	726.5	53.9	548	5	Q9W0G1	Q9W0G1 drosophila
8	633	47.0	331	5	Q9N109	Q9N109 brachiohisto
9	633	46.8	272	11	Q9N109	Q9N109 mus musculu
10	588	43.7	379	13	Q9N109	Q9N109 mus musculu
11	516	38.3	578	5	Q9W324	Q9W324 drosophila
12	516	38.3	827	5	Q96029	Q96029 drosophila
13	503	37.3	694	13	Q91870	Q91870 xenopus lae
14	500	37.1	597	13	Q91871	Q91871 xenopus lae
15	495.5	36.8	579	11	Q91307	Q91307 mus musculu
16	493.5	36.6	1647	5	Q9VW41	Q9VW41 drosophila

17	489.5	36.3	1767	5	Q9W4F5	Q9W4F5 drosophila
18	485.5	36.0	1767	5	Q24495	Q24495 drosophila
19	474	35.2	1337	4	Q15255	Q15255 homo sapien
20	471.5	35.0	1501	11	Q9W0U0	Q9W0U0 rattus norv
21	471.5	35.0	1863	11	Q64605	Q64605 rattus norv
22	470	34.9	1214	5	Q9VAL3	Q9VAL3 drosophila
23	469.5	34.9	593	13	Q90687	Q90687 gallus gall
24	469.5	34.9	597	11	Q64509	Q64509 mus musculu
25	468	34.7	1406	13	Q9W6V5	Q9W6V5 gallus gall
26	467	34.7	649	11	Q64641	Q64641 rattus norv
27	467	34.7	1216	11	Q62797	Q62797 rattus norv
28	465.5	34.5	1194	4	Q75870	Q75870 homo sapien
29	465	34.5	1194	11	Q9J1U0	Q9J1U0 mus musculu
30	464.5	34.5	1502	4	Q90M81	Q90M81 homo sapien
31	463	34.4	1405	4	Q60998	Q60998 mus musculu
32	463	34.4	1215	11	Q62884	Q62884 rattus norv
33	462	34.3	361	11	Q61373	Q61373 mus musculu
34	461.5	34.3	613	11	P81718	P81718 rattus norv
35	460.5	34.2	595	13	Q92124	Q92124 xenopus lae
36	460	34.1	372	4	Q90B75	Q90B75 homo sapien
37	460	34.1	405	4	Q90B70	Q90B70 homo sapien
38	460	34.1	1216	4	Q16427	Q16427 mus musculu
39	459	34.1	405	6	Q29570	Q29570 oryctolagus
40	459	34.1	1187	6	Q28613	Q28613 oryctolagus
41	458.5	34.0	326	11	Q9W022	Q9W022 mus musculu
42	458.5	34.0	1948	4	Q13332	Q13332 homo sapien
43	457.5	34.0	556	11	Q35128	Q35128 mus musculu
44	457.5	34.0	595	11	Q921G3	Q921G3 mus musculu
45	457.5	34.0	597	11	Q9R0V6	Q9R0V6 mus musculu

ALIGNMENTS

RESULT 1
Q9N004 PRELIMINARY: PRT: 414 AA.
AC Q9N004:
DT 01-OCT-2000 (PREMRELE, 15, Created)
DT 01-OCT-2000 (PREMRELE, 15, Last sequence update)
DT 01-DEC-2001 (PREMRELE, 19, Last annotation update)
DE 2150115.1 (PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 (EC 3.1.3.48)) (FRAGMENT).
GN PTPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartitidae; Homiidae; Homo.
OX NCBI_TaxID=9606;
BN [1]
SP SEQUENCE FROM N.A.
PA Wall M.
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR FMBL: AL133230; CAC00618.1; -
DR HSSP: P18031; IPTY.
DR InterPro: IPR000340; DS_phosphatase.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR002422; TYR_prot_phphatase.
DR PRINTS: PR00700; PRTPHPTASE.
DR SMART: SM00194; PRTP_DSPh; 1.
DR SMART: SM00194; PRTP_DSPh; 1.
DR PROSITE: PS00483; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00483; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00483; TYR_PHOSPHATASE_3; 1.
DR PROSITE: PS00483; TYR_PHOSPHATASE_4; 1.
DR PROSITE: PS00483; TYR_PHOSPHATASE_5; 1.
DR PROSITE: PS00483; TYR_PHOSPHATASE_6; 1.
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DR PROSITE: PS00483; TYR_PHOSPHATASE_14; 1.
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DR PROSITE: PS00483; TYR_PHOSPHATASE_26

KC H15SDH-EYE, AND RETINOH/ASTROMA;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC008244; AAH08244.1;
 KW Receptor.
 SO SOURCE: 187 AA; 45168 MW; 0F3F6220BA5A92CH CPO64;

Query Match 75.1%; Score 1011; DB 4; Length 387;
 Best Local Similarity 72.3%; Pred. No. 4e-87; 29; Indels 6; Gaps 3;
 Matches 185; Conservative 30; Mismatches 29;

OY 1 DPGGVAKIIPKRNKRNRYDVSPPDHRSIKLHQEDNDYINASTLIMPEAORSYLLTQGL 60
 DB 31 DPHRAKAFEPENPNRPVPEVSPYDHSRYKIQNAENDYINASTLVDEKORSYLLTQGL 90
 OY 61 PNTGHEWEMVWFKSRGVVMIINREKSGSLKQVQYQKEKEMFEENIKLITSPD 120
 DB 91 PNTGHEWEMVWFKSRGVVMIINREKSGSLKQVQYQKEKEMFEENIKLITSPD 149
 OY 121 IKSYIV--LELENTLTQETRELLHPHTTWPEEGVESPASFLNLFKVRSGSLSPDH 178
 DB 150 VKSYIVVHLQLEINSGSLFRTSHFTYITWPEEGVESPASFLNLFKVRSGSLSPDH 209
 OY 179 GPVAVHCSAGTIGSGTFLADTCLIMDKKQDSSVDIKKLLFMKPPMGIQIAVQIR 248
 DB 210 GPVAVHCSAGTIGSGTFLADTCLIMDKKQDSSVDIKKLLFMKPPMGIQIAVQIR 266
 OY 239 FSYAVIEGAKFTMGD 254
 DB 267 FSYAVIEGAKFTMGD 282

RESULT - 5

OY 0922E7 PRELIMINARY; PRT: 406 AA
 AC 0922E7;
 DT 01-DEC-2001 (TREMBLER). 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLER). 19, Last annotation update)
 DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID 10093
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC008269; AAH08269.1;
 KW Receptor.
 SO SOURCE: 406 AA; 47360 MW; DFB881DF3080DCC3 CPO64;

Query Match 74.5%; Score 1008; DB 11; Length 406;
 Best Local Similarity 71.5%; Pred. No. 6.2e-87;
 Matches 183; Conservative 38; Mismatches 29; Indels 6; Gaps 3;

OY 1 DPGGVAKIIPKRNKRNRYDVSPPDHRSIKLHQEDNDYINASTLIMPEAORSYLLTQGL 60
 DB 31 DPHRAKAFEPENPNRPVPEVSPYDHSRYKIQNAENDYINASTLVDEKORSYLLTQGL 90
 OY 61 PNTGHEWEMVWFKSRGVVMIINREKSGSLKQVQYQKEKEMFEENIKLITSPD 120
 DB 91 PNTGHEWEMVWFKSRGVVMIINREKSGSLKQVQYQKEKEMFEENIKLITSPD 149
 OY 121 IKSYIV--LELENTLTQETRELLHPHTTWPEEGVESPASFLNLFKVRSGSLSPDH 178
 DB 150 VKSYIVVHLQLEINSGSLFRTSHFTYITWPEEGVESPASFLNLFKVRSGSLSPDH 209
 OY 179 GPVAVHCSAGTIGSGTFLADTCLIMDKKQDSSVDIKKLLFMKPPMGIQIAVQIR 248
 DB 210 GPVAVHCSAGTIGSGTFLADTCLIMDKKQDSSVDIKKLLFMKPPMGIQIAVQIR 266

OY 239 FSYAVIEGAKFTMGD 254
 DB 267 FSYAVIEGAKFTMGD 282

RESULT 6

OY1BA4 PRELIMINARY; PRT: 322 AA.

ID OY1BA4;
 AC OY1BA4;
 DT 01-OCT-2000 (TREMBLER). 15, Created)
 DT 01-OCT-2000 (TREMBLER). 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLER). 19, Last annotation update)
 DE KATPP3 PROTEIN (FRAGMENT).
 OS Potamogeton nodosus (South American freshwater silurid).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squales; Hypnosquales; Pristigastera; Batoida;
 OC Myliobatiformes; Myliobatoidei; Potamogetonidae; Potamogeton.
 OX NCBI_TaxID=86373;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20219325; PubMed-10754074;
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
 RA "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
 RI divergence of tissue-specific isoform genes in the early evolution of
 vertebrates.";
 RT J. Mol. Evol. 50:302-311(2000).
 RL EMBL: AB033582; BAA95169.1;
 DR HSSP; P18031, 187J.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR003242; TYR_prot_phosphatase.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00194; PTPc; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase.
 FT NON_TER
 SO SOURCE: 322 AA; 36954 MW; B004572866F1197 CPO64;

Query Match 54.9%; Score 739; DB 13; Length 322;
 Best Local Similarity 75.0%; Pred. No. 1.4e-61;
 Matches 138; Conservative 22; Mismatches 22; Indels 2; Gaps 1;

OY 73 EOKSKGVMIINREKSGSLKQVQYQKEKEMFEENIKLITSPDHSPVAVVHSA316 130
 DB 1 EOKSRAIVMIINREKSGVCKEYKWNSTKIDMSYDTCNKLICHDVKSYYTVARLRL 60
 OY 131 ENLTQETRELLHPHTTWPEEGVESPASFLNLFKVRSGSLSPDHSPVAVVHSA316 190
 DB 61 QRTSTGKRELVHHTTWPEEGVESPASFLNLFKVRSGSLSPDHSPVAVVHSA316 120
 OY 191 KSGTFLADTCLIMDKKQDSSVDIKKLLFMKPPMGIQIAVQIR 250
 DB 121 KSGTFLADTCLIMDKKQDSSVDIKKLLFMKPPMGIQIAVQIR 180
 OY 251 LMD 254
 DB 181 LMD 184

RESULT 7
 OY0M0G1 PRELIMINARY; PRT: 548 AA.

ID OY0M0G1;
 AC OY0M0G1, OY0M0G2, OY79332;
 DT 01-MAY-2000 (TREMBLER). 13, Created)
 DT 01-MAY-2000 (TREMBLER). 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLER). 17, Last annotation update)
 DE PROTEIN-TYROSINE PHOSPHATASE 61F (FC 3.1.3.48) (PTPc1F PROTEIN)
 DR (CG9181 PROTEIN).


```

DB 740 DUMABPBPBPVIVHSAATGBCGCTTDTCT---SRIPIVGTATIPCTVFKIKISOPAY 786
OY 240 ITTADQIPCYAVIATPQA 248
DB 787 STOMDQVFFCHALITVA 805

RESULT 14
OY1870 PRELIMINARY: PRT: 694 AA.
ID OY1870
DT 01-NOV-1996 (TREMBLER 01, Created)
DT 01-NOV-1996 (TREMBLER 01, last sequence update)
DT 01-DEC-2001 (TREMBLER 19, last annotation update)
DE TYROSINE PHOSPHATASE
OS Xenopus laevis (African clawed frog).
PK PK00343 Met-344 Chod-343 of 1944, Vertebrata, Vertelostomi:
OC Amphibia: Batrachia: Anura: Mesobatrachia, Pipridae, Pipridae.
OC Xenopodinae: Xenopus.
OX NCBI_TaxID=8455.
RN [1]
RF SEQUENCE FROM N.A.
RC TISSUE-Ovary.
RA Del Vecchio R.L.;
RT "Characterization of two structurally related Xenopus laevis protein
   tyrosine phosphatases with homology to lipid binding proteins."
RL J. Biol. Chem 0-0-0(1994)
DR EMBL: L34098; AAA50778.1;
DR HSSP: Q06124; 25HP.
DR InterPro: IP0001251; CPAL_TRIO.
DR InterPro: IP0000487; TYR_phosphatase.
DR InterPro: IP0000442; TYL_Prot_Phphtase.
DR Pfam: PF00650; CRAL_TRIO.1.
DR Pfam: PF00102; Y_phosphatase.1.
DR PRINTS: PR00700; PRYPPHPTASE.
DR SMART: SM00194; PTPC.1.
DR SMART: SM00516; SEC14.1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolyase.
SQ SEQUENCE 694 AA: 79401 MW: 654059CA79HFA63H CKE64;

Query Match 37.1%; Score 563; DR 13; Length 694;
Best Local Similarity 41.5%; Pred No 6,5e-39;
Matches 110; Conservative 44; Mismatches 81; Indels 30; Gaps 7;

DB 6 VAKLQKNKPNRYPRVSPDHSPTKTL----HQPNCYTNASLIKMEFAQSYTLTGGPLP 61
OY 419 ISKSHNQKPNRYSPVCLQDSPPVKLQVSTDETYTYNASFDQYKKNAYIATGGPLP 478
DB 62 NQCGHFWBWDKSKOVYALNVKMKGSIKCAQYWDQKTKKIMEDT-----NKLK 115
OY 479 KLEDPWKKVWVWCKVLIYMTIKVLEKIKQYWMLEAKS---EDGHTLIKNIHL 545
DB 116 LISEDIKSYTYLEELNLTQETKEILHEHYITWPRGVPSPASPLNFKYKRESQSLIS 175
OY 536 LF-QQPK--LTHFVYVNGDHSVSAHYQVMSWPRGVKKSASAMIDRKIVNKHQAVAA 592
DB 176 -----PRHVVVNHGSGTSPSTPTLADPTLLIMKPKDSSVYTKVLLMP 274
OY 593 VVALMKAMTIGHFGAGFVVVNHGSGTSPSTPTLDTCT---SRIPIGVTVVLTQTKRMR 649
DB 225 KLRMGLQVATQGLKSYAVIATPQA 249
OY 650 TQAPSTGLTWQYTYTMAITEVQA 674
DB 650 TQAPSTGLTWQYTYTMAITEVQA 674

RESULT 14
OY1871 PRELIMINARY: PRT: 597 AA.
ID OY1871

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AC OY1871;
DT 01-NOV-1996 (TREMBLER 01, Created)
DT 01-NOV-1996 (TREMBLER 01, last sequence update)
DT 01-DEC-2001 (TREMBLER 19, last annotation update)
DE TYROSINE PHOSPHATASE
OS Xenopus laevis (African clawed frog).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Amphibia: Batrachia: Anura: Mesobatrachia, Pipridae, Pipridae.
OC Xenopodinae: Xenopus
OX NCBI_TaxID=8355;
RN [1]
RF SEQUENCE FROM N.A.
RC TISSUE-Ovary.
RA Del Vecchio R.L.;
RT "Characterization of two structurally related Xenopus laevis protein
   tyrosine phosphatases with homology to lipid binding proteins."
RL J. Biol. Chem 249 1849-1944(1994).
DR EMBL: L34099; AAA21728.1; -.
DR HSSP: P18052; TYPO.
DR InterPro: IP0001251; CPAL_TRIO.
DR InterPro: IP0000487; TYR_phosphatase.
DR InterPro: IF0000442; TYL_Prot_Phphtase.
DR Pfam: PF00650; CRAL_TRIO.1.
DR Pfam: PF00102; Y_phosphatase.1.
DR PRINTS: PR00700; PRYPPHPTASE.
DR SMART: SM00194; PTPC.1.
DR SMART: SM00516; SEC14.1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolyase.
SQ SEQUENCE 597 AA: 68843 MW: 62450EF718B0735 CRO64;

Query Match 37.1%; Score 500; DR 13; Length 597;
Best Local Similarity 41.1%; Pred No 1e-38;
Matches 109; Conservative 44; Mismatches 82; Indels 30; Gaps 7;

DB 6 VAKLQKNKPNRYPRVSPDHSPTKTL----HQPNCYTNASLIKMEFAQSYTLTGGPLP 61
OY 419 ISKSHNQKPNRYSPVCLQDSPPVKLQVSTDETYTYNASFDQYKKNAYIATGGPLP 381
DB 62 NQCGHFWBWDKSKOVYALNVKMKGSIKCAQYWDQKTKKIMEDT-----NKLK 115
OY 382 KLEDPWKKVWVWCKVLIYMTIKVLEKIKQYWMLEAKS---EDGHTLIKNIHL 438
DB 116 LISEDIKSYTYLEELNLTQETKEILHEHYITWPRGVPSPASPLNFKYKRESQSLIS 175
OY 439 LF-QQPK--LTHFVYVNGDHSVSAHYQVMSWPRGVKKSASAMIDHSQYKHQAVAA 495
DB 176 -----PRHVVVNHGSGTSPSTPTLADPTLLIMKPKDSSVYTKVLLMP 224
OY 496 VVALMKAMTIGHFGAGFVVVNHGSGTSPSTPTLDTCT---SRIPIGVTVVLTQTKRMR 552
DB 225 KLRMGLQVATQGLKSYAVIATPQA 249
OY 553 TQAPSTGLTWQYTYTMAITEVQA 577
DB 553 TQAPSTGLTWQYTYTMAITEVQA 577

RESULT 15
OY1871 PRELIMINARY: PRT: 579 AA.
ID OY1871
DT 01-NOV-1996 (TREMBLER 15, Created)
DT 01-DEC-2001 (TREMBLER 15, last sequence update)
DT 01-DEC-2001 (TREMBLER 19, last annotation update)
DE TYROSINE PHOSPHATASE
OS Mus musculus (Mouse).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathia: Muridae: Murinae: Mus.
OX NCBI_TaxID=10090;
RN [1]

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Matches 197: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GILPNTGIFHEWVWQKSGVWMLRWMEKSLKCAQYWPQKEKEKEMLEFDTNLKTLI 117
 58 GILPNTGIFHEWVWQKSGVWMLRWMEKSLKCAQYWPQKEKEKEMLEFDTNLKTLI 117
 DB 58 GILPNTGIFHEWVWQKSGVWMLRWMEKSLKCAQYWPQKEKEKEMLEFDTNLKTLI 117
 QY 118 SDPIKSYVLELELNTLQETRELLPHVYTWDPGVPSFASFLNPLKVRKSGSLSPD 177
 118 SDPIKSYVLELELNTLQETRELLPHVYTWDPGVPSFASFLNPLKVRKSGSLSPD 177
 DB 118 SDPIKSYVLELELNTLQETRELLPHVYTWDPGVPSFASFLNPLKVRKSGSLSPD 177
 QY 178 HGVVYVHCAGTRPSGTFTLADTCLLMOKRPPSSVDIKKVLLEMRKFMGLIOTADOL 237
 178 HGVVYVHCAGTRPSGTFTLADTCLLMOKRPPSSVDIKKVLLEMRKFMGLIOTADOL 237
 DB 178 HGVVYVHCAGTRPSGTFTLADTCLLMOKRPPSSVDIKKVLLEMRKFMGLIOTADOL 237
 QY 238 PFSYIAVECAKFTMD 254
 238 PFSYIAVECAKFTMD 254
 DB 238 PFSYIAVECAKFTMD 254

RESULT 3
 AAG78311
 ID AAG78311 standard; Protein: 321 AA.
 AC AAG78311;
 XX 20-NOV-2001 (first entry)
 DE human FTIB mutant G215S catalytic domain (PTP1B/c215S).
 XX protein tyrosine phosphatase; PTP1B; catalytic domain; human;
 KW type II diabetes; obesity; inhibition; insulin signalling regulator;
 KM mutant; moten.
 XX Homo sapiens
 OS Synthetic.
 XX Key location/Qualifiers
 FT Misc-difference 215 /note- "Ser replaces wild type Cys"
 XX W0200164939-A2.
 XX 07-SEP-2001
 XX 02-MAR-2001; 2001W0-SP0249
 XX 02-MAR-2000; 2000U0-0517170.
 XX (MORF-) MORPHOCHRM AG.
 XX Liu Y, Wang S, Zhang Z.
 XX WPT: 2001-582165/65.
 XX N-PSDB: AAI64150
 XX Identifying inhibitors or activators of enzymes, particularly of
 PT protein tyrosine phosphatase for treating diabetes or obesity comprises
 PT using inactive, but substrate-binding enzyme mutant.
 XX Disclosures: page 7; 24pp; English.

The sequence represents the amino acid sequence of the catalytic domain
 of the mutant of human protein tyrosine phosphatase 1B (PTP1B) designated
 PTP1B-215S. The mutant lacks catalytic activity but retains the ability
 to bind substrate and is used in the method of the invention. The
 invention relates to a novel method for the production of inhibitors or
 activators of an enzyme, the method is especially used to identify
 inhibitors of protein tyrosine phosphatase (PTP) and can be used for
 treatment of type II diabetes and obesity. The mechanism of action is
 therefore through inhibition of PTP, a regulator of insulin signalling
 and a key mediator in development of insulin resistance. The assay is
 simple, fast, homogeneous, accurate and inexpensive. Particularly it does
 not require an antibody (contrast known fluorescent polarisation methods)

CC and is easily adapted for high throughput screening.
 XX Sequence 321 AA;
 S2 Query Match 50.0%; Score 127, 38 22, Length 421;
 Best Local Similarity 100.0%; Pctd. No. 5, 5e 121;
 Matches 127: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPCVAVLPRKKNRKYRVSPTHSKIKLHGEINDYINSLIKMEFQNSYILTOSPL 60
 1 DEPCVAVLPRKKNRKYRVSPTHSKIKLHGEINDYINSLIKMEFQNSYILTOSPL 60
 DB 29 dfervakikpukunuyidvspfdhsrik;hgddyfnas;tkwcaqpsylltqpl 88
 29 dfervakikpukunuyidvspfdhsrik;hgddyfnas;tkwcaqpsylltqpl 88
 QY 61 IPTDGHFWHFWHWSKGVWMLRWMEKSLKCAQYWPQKEKEKEMLEFDTNLKTLI 120
 61 IPTDGHFWHFWHWSKGVWMLRWMEKSLKCAQYWPQKEKEKEMLEFDTNLKTLI 120
 DB 89 pntcqhllwewwqksrlqvmlurwckqsklcaq;wpqkeekemledlnklilised 148
 89 pntcqhllwewwqksrlqvmlurwckqsklcaq;wpqkeekemledlnklilised 148
 QY 121 IKSYYIV 127
 121 IKSYYIV 127
 DB 149 IKSYYIV 155

RESULT 4
 AAM48944
 ID AAM48944 standard; Protein: 323 AA.
 AC AAM48944;
 XX 26-OCT-1998 (first entry)
 DE Mutant human PTP1B tyrosine kinase phosphatase.
 XX Mutant human PTP1B tyrosine kinase phosphatase.
 KW mutant human PTP1B tyrosine kinase phosphatase; protease; SPA;
 KM scintillation proximity binding assay; diabetes; cancer;
 XX 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.
 XX Homo sapiens.
 OS Synthetic.
 XX Key location/Qualifiers
 FT Misc-difference 323 /note- "The residue is encoded by GAC, but it is
 FT not specified in the specification which
 FT gives a 322 residue protein"
 XX Misc-difference 251 /note- "changed from Cys in wild type to Ser in
 XX mutant"
 XX W09820156-A1.
 XX 14-MAY-1998.
 XX 03-NOV-1997; 97W0-CA00825.
 XX 04-NOV-1996; 96US-0030408.
 XX (MERI) MEPRK PROSST CANADA INC.
 XX Desmarais S, Ford-Hutchinson A, Friesen R, Gresser M.
 XX Kennedy B, Nicholson D, Ramchandran C, Skorey K.
 XX WPT: 1998-348103/30.
 XX Enzyme binding assay for detection of useful compounds - uses mutant
 FT form of wild-type enzyme, in which serine replaces cysteine at
 PT active site, to reduce interference from oxidising/alkylating agents
 XX Disclosures: pages 47-48, 63pp; English.

The present sequence represents a mutated human PTP1B tyrosine kinase
 phosphatase. The protein has a truncation (comprising residues 1-320)
 and single point mutant (where residue 251 is changed from cysteine to
 CC serine) when compared to the wild type PTP1B tyrosine kinase phosphatase.

02-MAR-1990: 900S-0487733.
 (HIOF-) APPL BIOTECHN INC.
 HUSKIN AM. H111 DE:
 WP1: 1991-281465/48.
 N-PSDB: AANI643.
 Vector contg. protein phosphotyrosyl phosphatase gene fragment
 for use in diagnosis of cancers, e.g. acute non-lymphocytic
 leukemia
 Claim 6: Fig 1: 79pp; English.
 A human placental cDNA library was screened with degenerate probes
 deduced from the partial amino acid sequence of the pypase 1b (see
 AM013653 and AM013654 for probe sequences). One recombinant
 bacteriophage hybridised to both probes and was shown to contain a
 3.2 kb fragment. The fragment was subcloned in pEMV2 and sequenced.
 The open reading frame was predicted to encode this 435 amino acid
 protein. The calculated mol wt is 49,966. PTPB is useful for
 treatment of AML, myelodysplastic syndrome and myeloproliferative
 disorders. See also AM013644-Q13654.

Sequence 435 AA:

Query Match 50.0%; Score 127; DB 12; Length 435;
 Best Local Similarity 100.0%; Freq. No. 7, 2e-121;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFCRCVAKLPKNNKNNRYRVSPPDHSRIKLIHQEDNDYINASLIKMEFAOSYILLTGPI 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 29 dfrctvarkipknkrnryrdsppdhsriklihqedndyinaslikmefasylitgpi 88
 QY 61 PNTGHHWEMWELKSGVYMLNFWMEKSLKCAQYWPQKEKEMIFEDNKLTLISEQ 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 89 pntcghwemwelsksgvymlnfwmekslkcaqywpqkeekemifednkltlised 148
 QY 121 IKSYYIV 127
 |||||||
 DB 149 Iksyyiv 155

RESULT 7

AAM51203
 ID AAM51203 standard; Protein: 435 AA.

AC AAM51203:

DI 19-DEC-2001 (first entry)

DE Human PTPB mutant D181A.

KW PTP: protein tyrosine phosphatase, tyrosine phosphorylated polypeptide;
 dephosphorylation; phosphotyrosine; human; PTPB; mutant; mutant.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FI Mismatch difference 181 /note- "Wild-type Asp substituted by Ala"

XX MO200161031-A2.

XX 23-AUG-2001.

XX 13-FEB-2001; 2001WO-US05180

XX 14-FEB-2000; 2000US-0181769.

XX

PA (CEPT-) CEPTK INC.
 XX Patent AJ, Cool DE:
 XX WP1: 2001-570570/64.

PT Screening assays to identify agents that alter protein tyrosine
 phosphorylation (PTP) binding to, and PTP-mediated catalytic
 dephosphorylation of phosphotyrosine peptide substrates

XX Example 1: Page 1: 79pp; English.

CC The invention relates to identifying agents which alter the interaction
 CC between a protein tyrosine phosphatase (PTP) and a tyrosine
 CC phosphorylated polypeptide using fluorescence energy signals. The methods
 CC are useful for performing screening assay to identify agents that alter
 CC PTP binding to and PTP mediated catalytic dephosphorylation of
 CC phosphotyrosine peptide substrates. The present sequence is that of a
 CC human PTPB D181A mutant.
 CC Note: The present sequence is not given in the specification but is
 CC derived from the wildtype human PTPB sequence (AAM51206) from
 CC Genbank (Accession Number: P18031). An alternative sequence for human
 CC PTPB is given in Figure 1 of the Specification (AAC78262).

XX Sequence 435 AA:

Query Match 50.0%; Score 127; DB 22; Length 435;
 Best Local Similarity 100.0%; Freq. No. 7, 2e-121;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFCRCVAKLPKNNKNNRYRVSPPDHSRIKLIHQEDNDYINASLIKMEFAOSYILLTGPI 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 29 dfrctvarkipknkrnryrdsppdhsriklihqedndyinaslikmefasylitgpi 88
 QY 61 PNTGHHWEMWELKSGVYMLNFWMEKSLKCAQYWPQKEKEMIFEDNKLTLISEQ 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 89 pntcghwemwelsksgvymlnfwmekslkcaqywpqkeekemifednkltlised 148
 QY 121 IKSYYIV 127
 |||||||
 DB 149 Iksyyiv 155

RESULT 8

AAM51204
 ID AAM51204 standard; Protein: 435 AA.

AC AAM51204:

DI 19-DEC-2001 (first entry)

DE Human PTPB mutant C215S.

KW PTP: protein tyrosine phosphatase, tyrosine phosphorylated polypeptide;
 dephosphorylation; phosphotyrosine; human; PTPB; mutant; mutant

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FI Mismatch difference 215 /note- "Wild-type Cys substituted by Ser"

XX MO200161031-A2.

XX 23-AUG-2001.

XX 13-FEB-2001; 2001WO-US05180.

XX 14-FEB-2000; 2000US-0181769.

XX (CEPT-) CEPTK INC.

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XX      Human AL, (AOL 143)
PT      phosphatase (PTP) binding for and PTP mediated catalytic
PT      dephosphorylation of phosphotyrosine peptide substrates
XX      Example 1: Page -- 79pp: English.
XX      The invention relates to identifying agents which alter the interaction
XX      between a protein tyrosine phosphatase (PTP) and a tyrosine
XX      phosphorylated polypeptide using fluorescence energy signals. The methods
XX      are useful for performing screening assay to identify agents that alter
XX      PTP binding to and PTP mediated catalytic dephosphorylation of
XX      phosphotyrosine peptide substrates. The present sequence is that of a
XX      human PTP1B cDNA mutant.
XX      Note: The present sequence is not given in the specification but is
XX      derived from the wild-type human PTP1B sequence (AA051206) from
XX      Genbank (Accession Number: P18031). An alternative sequence for human
XX      PTP1B is given in Figure 1 of the specification (AA078262).
XX      Sequence 435 AA:
XX
XX      Query Match: 50.0%; Score 127; DB 27; Length 435;
XX      Host Local Similarity 100.0%; Pred. No. 7.2e-121;
XX      Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 DFFGVAKLKKNNKRNKRDVSFFDHSRKLHQENDVINASLIKMEEAORSYLTGGPL 60
XX      29 dffgvaklkknnkrrnkrdvsffdhssrklhqendvinnaslikmeeaorsyltggpl 88
XX      61 PNTGHEFKEMVEQKSNVWNLNPNVEKRSIKCAAYWPAKFEREMIEYINRILTISED 120
XX      89 pntghefkemveqksnvwnlnpnvekrslkcaaywpaakeremieylnriltised 148
XX      121 IKSYYIV 27
XX      149 IKSYYIV 155
XX
XX      RESULT 10
XX      AA051206 standard: protein: 435 AA.
XX      AA051206:
XX      AC      AAM12006;
XX      AT      14 FEB 2001 (first entry)
XX      DE      Human PTP1B Genbank Accession Number P18031.
XX      KW      PTP1B protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
XX      dephosphorylation; phosphotyrosine; human; PTP1B.
XX      OS      Homo sapiens.
XX      PN      W020061001 A2;
XX      PR      24 AUG 2001.
XX      PT      14 FEB 2001; 2001W: 0500180.
XX      14 FEB 2001; 2000US: 017099.
XX      (CDB ) CDBTYR INT.
XX      Human AL, (AOL 143)
XX      W01: 2001 5/06/02/1.
XX      Reported assays to identify agents that alter protein tyrosine

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PT      phosphatase (PTP) binding for and PTP mediated catalytic
PT      dephosphorylation of phosphotyrosine peptide substrates
XX      Example 1: Page -- 79pp: English.
XX      The invention relates to identifying agents which alter the interaction
XX      between a protein tyrosine phosphatase (PTP) and a tyrosine
XX      phosphorylated polypeptide using fluorescence energy signals. The methods
XX      are useful for performing screening assay to identify agents that alter
XX      PTP binding to and PTP mediated catalytic dephosphorylation of
XX      phosphotyrosine peptide substrates. The present sequence is not given in
XX      the specification but is that of human PTP1B protein sequence taken from
XX      Genbank (Accession Number: P18031). The present sequence was used to
XX      generate mutants P18A (AA051203) and c215S (AA051204) as described in
XX      the specification.
XX      Note: An alternative sequence for human PTP1B is given in Figure 1 of
XX      the specification (AA078262).
XX      Sequence 435 AA:
XX
XX      Query Match: 50.0%; Score 127; DB 27; Length 435;
XX      Host Local Similarity 100.0%; Pred. No. 7.2e-121;
XX      Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 DFFGVAKLKKNNKRNKRDVSFFDHSRKLHQENDVINASLIKMEEAORSYLTGGPL 60
XX      29 dffgvaklkknnkrrnkrdvsffdhssrklhqendvinnaslikmeeaorsyltggpl 88
XX      61 PNTGHEFKEMVEQKSNVWNLNPNVEKRSIKCAAYWPAKFEREMIEYINRILTISED 120
XX      89 pntghefkemveqksnvwnlnpnvekrslkcaaywpaakeremieylnriltised 148
XX      121 IKSYYIV 127
XX      149 IKSYYIV 155
XX
XX      RESULT 10
XX      AA05848
XX      ID      AA05848 standard: protein: 435 AA.
XX      AC      AA05848;
XX      AT      25-Sep-2001 (first entry)
XX      DE      Human protein phosphatase 1B (PTP1B).
XX      KW      Human; protein phosphatase 1B; PTP1B; antisense; gene therapy;
XX      infection; inflammation; tumour; prophylaxis.
XX      OS      Homo sapiens.
XX      PN      US6261840-D1.
XX      PR      17-JUL-2001.
XX      PT      18-JAN-2000; 2000US: 0487368.
XX      18-JAN-2000; 2000US-0487368.
XX      (ISIS ) ISIS PHARM INC.
XX      CowSort LM, Wyatt J;
XX      WPI: 2001 432181/46.
XX      N-PSDB: MAD11946.
XX      New antisense compounds capable of modulating expression of human
XX      protein phosphatase 1B, useful for diagnosis, prophylaxis and treatment
XX      of diseases associated with expression of protein phosphatase
XX      Example 14: Column 55-60; 71pp: English.

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used as a local additive or preservative to increase storage capabilities. Sequences AM69016, 200024 and AM64453 are used in the course of the invention during the identification and characterisation of the protein and nucleotide sequences.

XX Sequence 59 AA:

Query Match 20.0%; Score 54; DB 21; Length 59;

Best Local Similarity 100.0%; Prod. No. 4,10-46; Mismatches 0; Indels 0; Gaps 0;

XX 58 YINASTLKPEFAKSYILTGLPTNTSHFEMVWEGKSPGVMLNRYEKGS 90
 |||
 DB 309 gplptcgaawemweweksgvmlnryekgs 53

RESULT 14

AM678263

ID AM678263 standard; Protein; 498 AA.

XX

XX AM678263

XX 19-FEB-2001 (first entry)

XX Novel human diastase or protein #28519.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX W0200175067 A2.

XX 11 OCT 2001.

XX 10 MAR 2001; 2001WO 0508641.

XX 4 MAR 2001; 2000US 040217.

XX 24 AUG 2000; 2000US 0049467.

XX (HUSE) HUSEG TM.

XX Human; RT; L10 Y; Lang Y1;

XX W01 2001 60982714.

XX N 2000; AASB/01.

XX New isolated polynucleotide and encoded polypeptides; useful in

XX diagnosis; forensic; gene mapping; identification of mutations

XX responsible for genetic disorders or other traits to assess biodiversity

XX Claim 20; SEQ ID No. 54878; 104pp; English.

XX The invention relates to isolated polynucleotide (1) and

XX polypeptide (11) sequences; (1) is useful as hybridisation probes,

XX and gene mapping; and in recombinant production of (11); the

XX polynucleotide are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes; (1) is useful in gene therapy techniques

XX to restore normal activity of (11) or to treat disease states involving

XX (11); (11) is useful for generating antibodies against it, detecting or

XX quantitating a polypeptide in tissue, as molecular weight markers and as

XX a food supplement; (11) and its binding partners are useful in medical

XX imaging of sites expressing (11); (1) and (11) are useful for treating

XX disorders involving aberrant protein expression or biological activity.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at <http://wipo.int/pat/published.pat.sequences>.

XX Sequence 498 AA:

Query Match 14.0%; Score 33; DB 22; Length 498;

Best Local Similarity 100.0%; Prod. No. 4,9e-25; Mismatches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 58 GPLPNTGSEFEMVWEGKSPGVMLNRYEKGS 90
 |||
 DB 309 gplptcgaawemweweksgvmlnryekgs 341

RESULT 14

AAG78263

ID AAG78263 standard; Protein; 251 AA.

XX

XX AAG78263

XX 19-FEB-2001 (first entry)

XX Human TCEP.

XX ptp; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;

XX dephosphorylation; phosphotyrosine; human; ptp1b; mouse; fruit fly;

XX yeast.

XX Homo sapiens.

XX W0200161031-A2.

XX 23-AUG-2001.

XX 13-FEB-2001; 2001WO 0505180.

XX 14-FEB-2000; 2000US 0181769.

XX (CIPR) CIPR INC.

XX Flint AL, Cool DE;

XX W01 2001-570570/64.

XX Screening assays to identify agents that alter protein tyrosine

XX phosphatase (PTP) binding to, and PTP mediated catalytic

XX dephosphorylation of phosphotyrosine peptide substrates

XX Disclosure; Fig 1; 79pp; English.

XX The invention relates to identifying agents which alter the interaction

XX between a protein tyrosine phosphatase (PTP) and a tyrosine

XX phosphorylated polypeptide using fluorescence energy signals. The methods

XX are useful for performing screening assay to identify agents that alter

XX PTP binding to and PTP mediated catalytic dephosphorylation of

XX phosphotyrosine peptide substrates. The present sequence is that of a

XX catalytic domain of a PTP for comparison with human ptp1b (AAG78263).

XX Sequence 251 AA:

Query Match 12.8%; Score 32; DB 22; Length 251;

Best Local Similarity 100.0%; Prod. No. 2,8e-24; Mismatches 0; Indels 0; Gaps 0;

XX 143 HFWTTPFQVPEPASFNLKRVKESST 174
 |||
 DB 141 hfwtpfqpypspstlnlkrvkst 172

RESULT 15

GenCore version 4.5
Copyright (c) 1993 - 2000 Compygen Ltd

OM protein - protein search, using sw model

Run On: June 18, 2002, 15:00:15 : Search time 19.23 seconds
(without alignments)
1254 two million n-11 updates/sec

Title: US-09-788-626-2
Perfect score: 254
Sequence: 1 DEPCVAVALKTKKNPPYP DQPSYLVATFGAKFMGD 254

Scoring table: Gapop 60.0 / Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size: 0 283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: FIR-7114
1: PIR1
2: PIR2
3: PIR3
4: PIR4

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the full score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	50.0	435	1	TPHUN1 protein-tyrosine-p
2	78	30.7	432	1	A34845 protein-tyrosine-p
3	64	25.2	432	1	IN0317 protein-tyrosine-p
4	55	21.7	356	2	JM0049 protein-tyrosine-p
5	42	12.6	363	1	S14294 protein-tyrosine-p
6	32	12.5	387	1	A60345 protein-tyrosine-p
7	32	12.6	415	1	A33899 protein-tyrosine-p
8	30	11.8	382	1	A38191 protein-tyrosine-p
9	16	6.3	535	2	A46101 protein-tyrosine-p
10	16	6.3	548	2	A46101 protein-tyrosine-p
11	14	5.5	377	1	A48711 protein-tyrosine-p
12	13	5.1	549	2	S53427 protein-tyrosine-p
13	13	5.1	585	2	A46209 protein-tyrosine-p
14	13	5.1	593	2	JN0805 protein-tyrosine-p
15	13	5.1	593	2	JN5167 protein-tyrosine-p
16	13	5.1	593	1	A55651 protein-tyrosine-p
17	13	5.1	597	1	A53593 protein-tyrosine-p
18	13	5.1	656	1	A55574 protein-tyrosine-p
19	13	5.1	656	1	JC1263 protein-tyrosine-p
20	12	4.7	694	2	A33978 protein-tyrosine-p
21	12	4.7	926	1	A41105 protein-tyrosine-p
22	11	4.3	2294	2	S71626 protein-tyrosine-p
23	11	4.3	2452	2	S71626 protein-tyrosine-p
24	11	4.3	2466	2	S71626 protein-tyrosine-p
25	11	4.3	2490	2	A54971 protein-tyrosine-p
26	10	3.9	256	2	A40169 protein-tyrosine-p
27	10	3.9	256	2	T06536 protein-tyrosine-p
28	10	3.9	332	2	T06536 protein-tyrosine-p
29	10	3.9	444	2	T12869 hypothetical prote

30	10	3.9	352	2	T20729 hypothetical prote
31	10	3.9	360	1	JH0692 protein-tyrosine-p
32	10	3.9	365	2	T25917 hypothetical prote
33	10	3.9	374	2	F88712 protein-tyrosine-p
34	10	3.9	398	2	S33446 hypothetical prote
35	10	3.9	398	2	T33446 protein-tyrosine-p
36	10	3.9	398	2	T08716 protein-tyrosine-p
37	10	3.9	593	1	A42690 protein-tyrosine-p
38	10	3.9	597	2	B53978 hypothetical prote
39	10	3.9	597	2	T21883 hypothetical prote
40	10	3.9	621	2	T21090 hypothetical prote
41	10	3.9	624	2	T19630 probable protein
42	10	3.9	668	2	T13417 hypothetical prote
43	10	3.9	1026	2	T19631 hypothetical prote
44	10	3.9	1156	2	T23308 protein-tyrosine p
45	10	3.9	1262	1	B48758

ALIGNMENTS

RESULT 1
TPHUN1
protein-tyrosine phosphatase (EC 3.1.3.48), nonreceptor type 1 [validated] - human
N:Alternate names: phosphotyrosine phosphatase 1B, long form; protein-tyrosine phosph
N:Contains: protein-tyrosine phosphatase, nonreceptor type 1, membrane-bound form; pr
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence, revision 07-Apr-1994 #text, change 15-Sep-2000
C:Accession: A35942; 159169; 179576; S15849; A33897; A37275
R:Chernoff, J.; Schievella, A.R.; Joshi, C.A.; Erikson, R.L.; Neel, B.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 2735-2739, 1990
A:Title: Cloning of a cDNA for a major human protein-tyrosine phosphatase.
A:Reference number: A35942; M01D:30207272
A:Accession: A35992
A:Molecule type: mRNA
A:Residues: 1-435 <CHP>
A:Cross-references: GB:M1724; NIH:q190741; EMBL:AA60223.1; PIR:q190742
A:Authors: Lawrence, G.B.; Johnson, K.A.; Lawrence, J.B.; Johnson, G.; Brunkin, A.; Green, N
R.; Brown-Shiner, S.; Johnson, K.A.; Lawrence, J.B.; Johnson, G.; Brunkin, A.; Green, N
Proc. Natl. Acad. Sci. U.S.A. 87, 5148-5152, 1990
A:Title: Molecular cloning and chromosome mapping of the human gene encoding protein
A:Reference number: 159169; M01D:90311360
A:Accession: 159169
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA; mRNA
A:Residues: 1-435 <CHP>
A:Cross-references: GB:M33689; NIH:q190271; EMBL:AA60157.1; PIR:q190272
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 165-435 <CHP>
A:Cross-references: GB:M33684; NIH:q190271; EMBL:AA60158.1; PIR:q190279
R:Fallon, C.J.; Lai, D.S.Y.; Chida, H.P.; Houlet, L.; Tong, D.H.
Biochem. J. 276, 315-323, 1991
A:Title: Purification and characterization of a higher-molecular mass form of protein
A:Reference number: S15849; M01D:91264781
A:Accession: S15849
A:Molecule type: protein
A:Residues: 1-821 (80-92, 94-99, 101-123, 130-180)
R:Charbonneau, H.; Tonks, N.K.; Kumar, S.; Hunter, T.; Cohen, P.; Hattaylock, M.; Cool, D.E.; KT
Proc. Natl. Acad. Sci. U.S.A. 86, 5252-5256, 1989
A:Title: Human placenta protein-tyrosine phosphatase: amino acid sequence and relation
A:Reference number: A33897; M01D:89315775
A:Accession: A33897
A:Molecule type: protein
A:Residues: 1-321 <CHAS>
R:Barford, D.; Flint, A.J.; Tonks, N.K.
submitted to the Brookhaven Protein Data Bank, September 1994
A:Reference number: A54879; PDB:2HNP
A:Contents: annotation; X-ray crystallography, 2.8 angstroms; residues 5-282
R:Barford, D.; Flint, A.J.; Tonks, N.K.
Science 263, 1397-1404, 1994
A:Title: Crystal structure of human protein-tyrosine phosphatase 1B.
A:Reference number: A58904; M01D:94174273

RESULT 4
 JMW0049
 protein-tyrosine-phosphatase (EC 3.1.3.48) 1 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #lex_change 03-Dec-1999
 C:Accession: JMW0049
 R:Jung, E.J.; Kane, Y.S.; Kim, C.W.
 Biochem. Biophys. Res. Commun. 246: 219-242, 1998
 A:Title: Multiple phosphorylation of chicken protein tyrosine phosphatase 1 and human p115^{cas} by protein-tyrosine phosphatase homologs
 A:Reference number: JMW049; MUID:9262948
 A:Accession: JMW0049
 A:Molecule type: mRNA
 A:Residues: 1-356 <CHN>
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1, protein tyrosine phosphatase
 C:Keywords: phosphatase; phosphatase; hydrolyase
 F:27-254/Domain: protein-tyrosine phosphatase homolog <PPs>
 F:27-254/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.7%, Score 55, DB 2, Length 356;
 Host Local Similarity 100.0%; Pred. No. 30-45;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 NQYVNSTKMEEDNRSYTTGGELFNTGHRWVWDEKSPVVMNRVMEKGS 90
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 51 NDYVNSTKMEEDNRSYTTGGELFNTGHRWVWDEKSPVVMNRVMEKGS 105

RESULT 5
 S14294
 protein-tyrosine-phosphatase (EC 3.1.3.48) 11A - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #lex_change 10-Sep-1999

C:Accession: S14294; S21831
 R:Swanup, G.; Kamakura, S.; Kadha, V.; Rama, V.
 FEBS Lett. 280: 65-69, 1991

A:Title: Molecular cloning and expression of a protein-tyrosine phosphatase showing homology to the human data library, April 1991

A:Reference number: S14294; MUID:31184432

A:Accession: S14294

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-363 <SWA>

A:Cross-references: GB:X58828; NID:476945; E15N:CAA11633.1; P1D:456496

R:Swanup, G.; Kamakura, S.; Kadha, V.; Rama, V.
 Submitted to the EMBL data library, April 1991

A:Reference number: S21831

A:Accession: S21831

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-363 <SWA2>

A:Cross-references: JMW:K58828; NID:476945; P1D:CAA11633.1; P1D:456496

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein tyrosine phosphatase

C:Keywords: alternative splicing; DNA binding; phosphoprotein; phosphoric monoester hydrolase

F:42-264/Domain: protein-tyrosine phosphatase intermediate #status predicted

F:216/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:222/Binding site: substrate phosphate (Arg) #status predicted

Query Match 12.6%, Score 32, DB 1, Length 363;
 Best Local Similarity 100.0%; Pred. No. 5-7e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 HHHTTWDPGVPSPASFLNFKVRESGS 174
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 174 HHHTTWDPGVPSPASFLNFKVRESGS 205

RESULT 6
 A60345
 protein-tyrosine-phosphatase (EC 3.1.3.48) 11A - human

C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1999 #sequence_revision 02-May-1994 #lex_change 24-Apr-1998

C:Accession: A60345; B60345

R:Champion-Arnaud, P.; Gesnel, M.C.; Foulkes, N.; Konstin, C.; Sassone-Corsi, P.; Brea
 Oncogene 6, 1203-1209, 1991

A:Title: Activation of transcription via AP-1 or CREB regulatory sites is blocked by

A:Reference number: A60345; MUID:91319401

A:Accession: A60345

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-367 <CHN>

A:Accession: B60345

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 348-387 <CH2>

C:Genetics:

A:Gene: GDB:PTPN2; PTP

A:Cross-references: GDB:128098; OMIM:176887

A:Map position: 18p11.22-18p11.21

A:Initons: 347/2, 381/2

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein tyrosine phosphatase

C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; Tyr

F:42-264/Domain: protein-tyrosine phosphatase intermediate #status predicted

F:216/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:222/Binding site: substrate phosphate (Arg) #status predicted

Query Match 12.6%, Score 32, DB 1, Length 387;
 Best Local Similarity 100.0%; Pred. No. 6-1e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 HHHTTWDPGVPSPASFLNFKVRESGS 174
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 174 HHHTTWDPGVPSPASFLNFKVRESGS 205

RESULT 7

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 2 - human

N:Alternative names: protein-tyrosine-phosphatase, T-cell specific

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence_revision 02-May-1994 #lex_change 07-May-1999

C:Accession: A33899; C60345; A45742

R:Cool, D.E.; Tonks, N.K.; Charbonneau, H.; Walsh, K.A.; Fischer, E.H.; Krebs, E.G.
 Proc. Natl. Acad. Sci. U.S.A. 86: 5257-5261, 1989

A:Title: cDNA isolated from a human T-cell library encodes a member of the protein-ty

A:Reference number: A33899; MUID:89315776

A:Accession: A33899

A:Molecule type: mRNA

A:Residues: 1-415 <COO>

A:Cross-references: GB:M25393

R:Champion-Arnaud, P.; Gesnel, M.C.; Foulkes, N.; Konstin, C.; Sassone-Corsi, P.; Brea

Oncogene 6, 1203-1209, 1991

A:Title: Activation of transcription via AP-1 or CREB regulatory sites is blocked by

A:Reference number: A60345; MUID:91319401

A:Accession: C60345

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 348-415 <CHN>

R:Johnson, C.V.; Cool, D.E.; Glanville, M.H.; Green, N.; Fischer, E.H.; Broskin, A.; H

Genomics 16, 619-629, 1993

A:Title: Isolation and mapping of human T-cell protein tyrosine phosphatase sequences

Onc.

A:Reference number: A45742; MUID:93315152

A:Accession: A45742

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 115-125/160 170/240-241/413 415 <COH>

C:Comment: This protein and protein-tyrosine-phosphatase 11A are produced from the sa

C:Genetics:

A:Gene: GDB:PTPN2; PTP

A:Cross-references: GDB:128098; OMIM:176887

A:Map position: 18p11.22-18p11.21

A:Initons: 120/3, 165/3, 235/3, 347/2

A:Note: List of Initons may be incomplete

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein tyrosine pho

F:287/binding site: substrate phosphate (Arg) #status predicted

Query Match 5.58; Score 14; DB 1; Length 377;

Best Local Similarity 100.0%; Pred. No. 1,6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 182 VHVHCSAGTGR 195

DB 278 VHVHCSAGTGR 291

RESULT 12

S53427 protein-tyrosine phosphatase (EC 3.1.3.48), probable receptor type PTPB7 splice form

C:Species: Mus musculus (house mouse)

C:Date: 31-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1998

C:Accession: S53427

C:Keywords: protein-tyrosine phosphatase, receptor type PTPB7, protein tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: A novel receptor type protein-tyrosine phosphatase with a single catalytic domain

A:Reference number: S53427; M01D:0514232

A:Accession: S53427

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-549 <SHS>

C:Supramiliary: protein-tyrosine phosphatase, receptor type PTPB7, protein tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

Query Match 5.18; Score 13; DB 2; Length 549;

Best Local Similarity 100.0%; Pred. No. 0.00021;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 179 GPVVHCSAGTGR 191

DB 474 GPVVHCSAGTGR 486

RESULT 13

A46209 protein-tyrosine phosphatase (EC 3.1.3.48), nonreceptor type II - mouse

N:Alternate names: SH-PTP2; SH2-containing phosphotyrosine phosphatase; Syt

C:Species: Mus musculus (house mouse)

C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Apr-1998

C:Accession: A46209

C:Keywords: protein-tyrosine phosphatase, receptor type PTPB7, protein tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: A46209; M01D:93206094

A:Accession: A46209

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-585 <FENS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: A46209; M01D:93206094

A:Accession: A46209

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-585 <FENS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: A46209; M01D:93206094

A:Accession: A46209

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-585 <FENS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

DB 457 GPVVHCSAGTGR 469

RESULT 14

JN0805

protein-tyrosine phosphatase (EC 3.1.3.48), nonreceptor type II - human

N:Alternate names: SHP-3; protein-tyrosine phosphatase SHP-2; PTPB2; PTPB2; SH-PTP2;

C:Species: Homo sapiens (man)

C:Date: 10-Mar-1994 #sequence_revision 19-May-1994 #text_change 21-Jul-2000

C:Accession: JN0805; A46210; A47386; A47244; S27398; C44929; S31767

C:Keywords: protein-tyrosine phosphatase, receptor type PTPB2, human protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: JN0805; M01D:94029983

A:Accession: JN0805

A:Molecule type: mRNA

A:Residues: 1-593 <DBNS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: JN0805; M01D:94029983

A:Accession: JN0805

A:Molecule type: mRNA

A:Residues: 1-593 <DBNS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: JN0805; M01D:94029983

A:Accession: JN0805

A:Molecule type: mRNA

A:Residues: 1-593 <DBNS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: JN0805; M01D:94029983

A:Accession: JN0805

A:Molecule type: mRNA

A:Residues: 1-593 <DBNS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: JN0805; M01D:94029983

A:Accession: JN0805

A:Molecule type: mRNA

A:Residues: 1-593 <DBNS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: JN0805; M01D:94029983

A:Accession: JN0805

A:Molecule type: mRNA

A:Residues: 1-593 <DBNS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: JN0805; M01D:94029983

A:Accession: JN0805

A:Molecule type: mRNA

A:Residues: 1-593 <DBNS>

C:Supramiliary: protein-tyrosine phosphatase, nonreceptor type 6, protein-tyrosine phosphatase, alternative splicing, brain, phosphoprotein, phosphatase, monomeric hydrolase

F:307-528/Domain: protein-tyrosine phosphatase (am-10); PTPB7

F:480/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:486/binding site: substrate phosphate (Arg) #status predicted

A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein tyrosine kinase

A:Reference number: JN0805; M01D:94029983

A:Accession: JN0805

A:Molecule type: mRNA

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 15:00:15 ; Search time 11.07 seconds

(without alignments)
888.416 Million cell updates/sec

Title: us-09-788-626-2

Perfect score: 254

Sequence: 1 DFFPRVAKLEKRNPNFYPD

AL10NMN1S

Scoring table: 0.160

Gapop 60.0 / Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	50.0	435	1	PTN1_HUMAN
2	79	31.1	432	1	PTN1_MOUSE
3	78	30.7	432	1	PTN1_RAT
4	56	22.0	434	1	PTN1_CHICK
5	32	12.6	415	1	PTN2_RAT
6	32	12.6	415	1	PTN2_HUMAN
7	30	11.8	377	1	PTN2_MOUSE
8	14	5.1	377	1	PTN2_DICDI
9	14	5.1	377	1	PTN3_MOUSE
10	13	5.1	593	1	PTN3_HUMAN
11	13	5.1	593	1	PTN3_MOUSE
12	12	5.1	989	1	PTN4_HUMAN
13	12	4.7	926	1	PTN4_MOUSE
14	11	4.3	2485	1	PTN7_HUMAN
15	10	3.9	360	1	PTN7_MOUSE
16	10	3.9	360	1	PTN9_HUMAN
17	10	3.9	593	1	PTN9_MOUSE
18	10	3.9	1026	1	PTN9_HUMAN
19	10	3.9	1422	1	PTN9_MOUSE
20	10	3.9	2314	1	PTN9_HUMAN
21	10	3.9	2314	1	PTN9_MOUSE
22	10	3.9	365	1	PTN5_RAT
23	9	3.5	537	1	PTN5_HUMAN
24	9	3.5	537	1	PTN5_MOUSE
25	9	3.5	541	1	PTN6_HUMAN
26	9	3.5	541	1	PTN6_MOUSE
27	9	3.5	845	1	PTN6_HUMAN
28	9	3.5	913	1	PTN3_HUMAN
29	9	3.5	1630	1	PTN1_MOUSE
30	8	3.1	521	1	PTN1_MOUSE
31	8	3.1	1238	1	PTN1_MOUSE
32	8	3.1	1337	1	PTN1_MOUSE
33	7	2.8	109	1	PTN4_STYPL

34	7	2.8	110	1	PTN3_STYPL
35	7	2.8	116	1	PTN3_STYPL
36	7	2.8	151	1	SP2C_STYPL
37	7	2.8	194	1	HIS7_MOUSE
38	7	2.8	332	1	THPA_HAEN
39	7	2.8	335	1	PTN1_YEAST
40	7	2.8	417	1	ASP_MOUSE
41	7	2.8	501	1	CRP5_MOUSE
42	7	2.8	507	1	GAG_STYPL
43	7	2.8	699	1	PTN1_MOUSE
44	7	2.8	700	1	PTN1_MOUSE
45	7	2.8	796	1	PTN1_MOUSE

RESULT	1	STANDARD	PRT	435 AA
PTN1_HUMAN				
ID	PTN1_HUMAN			
AC	P18031; Q9NQ04; Q9H0V9;			
DT	01-NOV-1990 (rel. 16, Created)			
DT	01-NOV-1990 (rel. 16, Last sequence update)			
DT	01-MAR-2002 (rel. 41, Last annotation update)			
DE	Protein-tyrosine phosphatase, non-receptor type 1 (EC 3.1.3.48)			
DE	(Protein-tyrosine phosphatase 1b) (PTP-1b).			
CN	PTN1 OR PTP1b.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N A			
RC	TISSUE=Placenta;			
KX	MDLINE=90207272; PubMed=2157211;			
RA	Chernoff J., Schiewella A.R., Jost C.A., Erikson R.L., Neel B.G.;			
PT	"Cloning of a cDNA for a major human protein-tyrosine phosphatase."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2745-2749(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
KX	MDLINE=9011163; PubMed=2161224;			
RA	Brown-Shmer S., Johnson K.A., Lawrence J.B., Johnson C.			
RT	"Molecular cloning and chromosome mapping of the human gene encoding protein phosphotyrosyl phosphatase 1b." (1990).			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:5148-5152(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	DeJonghe P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babington A.K., Hagley C.L.,			
RA	Bailey J., Bartow K.F., Bates K.N., Healy L.M., Heare D.M.,			
RA	Beggs O.F., Bird C.P., Blakey S.F., Bridgman A.M., Brown A.J.,			
RA	Buck D., Burdill W., Butler A.P., Garder C., Garner N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Copley V.E., Collier R.E., Doherty P., Gaby N.R.,			
RA	Conlon A., Coville G.J., Dearden R., Dhami P., Dunn M.,			
RA	Ellington A.C., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Griffiths M.N.D., Griffiths M.N.D., Gwilliam R., Hall R.R.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.T.,			
RA	Huckle E., Hunt A.P., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvasaisto M.H., Leverisha M., Lloyd G., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.H., Martin S.L., McCormack L., McKay K., Murray A.A.,			
RA	Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,			
RA	Phillimore R.T.F., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Serna H.K., Snowdon K., Sims S.,			
RA	Smyke C.D., Smith M.L., Soderlund C., Steward C.A., Sullivan J.F.,			
RA	Swann M., Symons N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whitehead S.T., Whitaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilming L., Wray F.W., Hubbard T., Durbin R.M., Bentley D.F., Beck S.,			

GN PTEN1.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Testis.
 RX MEDLINE=92328784; PubMed 1378268;
 RA Miyasaka H., Li S.S.L.
 RT "The cDNA cloning, nucleotide sequence and expression of an
 RL intracellular protein tyrosine phosphatase from mouse testis."
 RL Biochem. Biophys. Res. Commun. 185:818-825(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Liao K., Lane M.D.
 RL Submitted (Apr-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Park K., Hyun S.
 RL Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 102-213 FROM N.A.
 RX STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE=95134332; PubMed 7832766;
 RA Hendriks W., Schepens J., Houtman G., Zecunen P., Wieringa B.
 RT "A novel receptor-type protein tyrosine phosphatase with a single
 RL catalytic domain is specifically expressed in mouse brain."
 RL Biochem. J. 405:499-504(1995).
 RN [5]
 RP SEQUENCE OF 161-432 FROM N.A.
 RA Strassberg R.
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED TO THE ENDOPLASMIC RETICULUM VIA
 CC ITS C-TERMINAL DOMAIN WITH ITS PHOSPHATASE DOMAIN ORIENTED TOWARDS
 CC THE CYTOSOL (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN TESTIS. ALSO FOUND IN KIDNEY,
 CC SPLEEN, MUSCLE, LIVER, HEART AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M97590; - NOT ANNOTATED CDS.
 DR EMBL: LA0595; AAA64615.1; -
 DR EMBL: U24700; AA98605.1; -
 DR EMBL: Z23057; CA880592.1; -
 DR EMBL: H0005729; AA005729.1; -
 DR EMBL: J06317; J06317.
 DR HSSP: P18031; 1PHY.
 DR MCD: M3197805; 1PHY.
 DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR000347; TYF_phosphatase.
 DR InterPro: IPR000242; TYF_prot_phosphatase.
 DR Pfam: PF00102; Y_phosphatase.1.
 DR PRINTS: PR00700; PR1PHPHASE.
 DR SMART: SM00194; PTpc.1.
 DR SMART: SM00112; PTpc_DSPc.1.
 DR PROSITE: PS00364; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 DR HYDROLASE.
 FT DOMAIN 40 288 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 215 215 BY SIMILARITY.

FT CONFLICT 48 48 D -> Y (IN REF. 1).
 FT CONFLICT 104 104 S -> P (IN REF. 1).
 FT CONFLICT 173 173 H -> P (IN REF. 2).
 FT CONFLICT 266 266 G -> H (IN REF. 2).
 FT CONFLICT 405 405 H -> K (IN REF. 1).
 FT SEQUENCE 432 AA. 49593 MD. 48432264C288C48 CIRC64.
 Query Match 31.1%; Score 79; DH 1; Length 432;
 Best Local Similarity 100.0%; Pred. No. 7,9e-76;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 6 VAKLEPKNNRNYRQVSPEDHSRIKLHEDNDYINSLIKMEEAQSYILTPGLPTG 65
 34 VAKLEPKNNRNYRQVSPEDHSRIKLHEDNDYINSLIKMEEAQSYILTPGLPTG 93
 OY 66 HFEWVWFGKSKGVMLNR 84
 94 HFEWVWFGKSKGVMLNR 112
 RESULT 3
 ID PTN1_RAT STANDARD; PRT; 432 AA.
 AC P20417;
 DT 01-FEB-1991 (Ref. 17, created)
 DT 01-FEB-1991 (Ref. 17, last sequence update)
 DT 15-OCT-2001 (Ref. 40, last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 1 (Ref 3,1,3,48)
 DE (Protein-tyrosine phosphatase 1B) (PTP-1B).
 GN PTEN1.
 OS Mus musculus (Mus).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Brain;
 RX MEDLINE=90160354; PubMed=2154749;
 RA Guan K., Han B.S., Watson S.J., Goshen K.L., Dixon J.E.
 RT "Cloning and expression of a protein tyrosine phosphatase."
 RL Efec. Natl. Acad. Sci. U S A. 87:1501-1505(1990).
 CC -1- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED TO THE ENDOPLASMIC RETICULUM VIA
 CC ITS C-TERMINAL DOMAIN WITH ITS PHOSPHATASE DOMAIN ORIENTED TOWARDS
 CC THE CYTOSOL.
 CC -1- TISSUE SPECIFICITY: FOUND IN SEVERAL TISSUES INCLUDING CENTRAL
 CC NERVOUS SYSTEM, LIVER AND KIDNEY. A HIGH LEVEL OF EXPRESSION WAS
 CC FOUND IN THE HIPPOCAMPUS.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M33962; AAC79516.1; -
 DR PIR: A34845; A34845.
 DR HSSP: P18031; 1PHY.
 DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR000347; TYF_phosphatase.
 DR InterPro: IPR000242; TYF_prot_phosphatase.
 DR Pfam: PF00102; Y_phosphatase.1.
 DR PRINTS: PR00700; PR1PHPHASE.
 DR SMART: SM00194; PTpc.1.
 DR SMART: SM00112; PTpc_DSPc.1.
 DR PROSITE: PS00364; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.

DR InterPro: IPR000487; Tyr_phosphatase.
 DR InterPro: IPR000487; Tyr_phosphatase.
 DR Pfam: PF00102; Y_phosphatase_1.
 DR PRINTS: PR00700; PRTPHPTASE.
 DR SMART: SM00194; PTPase_1.
 DR PROSITE: PS00483; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase; DNA-binding.
 FT DOMAIN 42 286 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 216 216 BY SIMILARITY.
 FT DNA_BIND 326 359 BASIC MOTIF (POTENTIAL).
 SQ SEQUENCE 363 AA: 42346 MW: 84170346.6024715 CRC64.

Query Match 12.6%; Score 32; FR: 1; Length 363;
 Best Local Similarity 100.0%; Pred. No. 4; 36-26;
 Matches 32, Conservative 0, Mismatches 0, Gaps 0.

DB 143 HHHYTTWPDGVESPASPLNLFKVKESGSL 174
 174 HHHYTTWPDGVESPASPLNLFKVKESGSL 205

RESULT 6
 PIN2_HUMAN STANDARD; PRT; 415 AA.
 AC P17706; Q96HR2;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 2 (EC 3.1.3.48) (T-cell protein-tyrosine phosphatase) (PTP2).
 GN PTPN2 OR PTP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE: T-cell;
 RX MIM: 603157; PubMed=7246150;
 RA "Cool B., Frank N., Chabbert-Vaut H., Walsh K., Fischer V.H., Krebs J.G.; cDNA isolated from a human T-cell library encodes a member of the protein-tyrosine-phosphatase family";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:5257-5261 (1989)
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92115688; PubMed=1731319;
 RA "Moshiger B. Jr., Tillmann H., Westphal H., Tremblay M.L.; Cloning and characterization of a mouse cDNA encoding a cytoplasmic protein-tyrosine phosphatase";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:499-503 (1992)
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PTPB).
 RC TISSUE: Eye;
 RA Strausberg P.; submitted (May-2001) to the FMR1/GenBank/EMBL databases.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 2; ISOFORMS: PTPA AND PTPB (SHOWN HERE), ARE PROTECTED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PTPA ISOFORM IS PROBABLY THE MAJOR PTP EXPRESSED IN HUMAN TISSUES. PTPB ISOFORM WAS FOUND IN T-CELLS AND IN PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.

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DR EMBL: M25393; AAA65997.1; -
 DR EMBL: M61478; -; NOT_ANNOTATED_CDS.
 DR EMBL: AC008244, AA008244.1, -
 DR F1R: A33899; A33899.
 DR HSSP: P18031; 1PTV.
 DR MIM: 176887; -
 DR InterPro: IPR000487; Tyr_phosphatase
 DR InterPro: IPR000487; Tyr_prot_phosphatase.
 DR Pfam: PF00102; Y_phosphatase_1.
 DR PRINTS: PR00700; PRTPHPTASE.
 DR SMART: SM00194; PTPase_1.
 DR PROSITE: PS00483; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase; Y-cell; Alternative splicing.
 FT DOMAIN 42 286 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 216 216 BY SIMILARITY.
 FT VARSPLIC 382 415 WYMDPTKMGPMSTVIGAVGMPFFQGNL -> PRL TDT (IN ISOFORM PTPA).
 SQ SEQUENCE 415 AA: 48528 MW: 93969444.058608 CRC64.

Query Match 12.6%; Score 32; DB 1; Length 415;
 Best Local Similarity 100.0%; Pred. No. 5; 66-26;
 Matches 32, Conservative 0, Mismatches 0, Gaps 0.

DB 143 HHHYTTWPDGVESPASPLNLFKVKESGSL 174
 174 HHHYTTWPDGVESPASPLNLFKVKESGSL 205

RESULT 7
 PIN2_MOUSE STANDARD; PRT; 382 AA.
 AC Q06180;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 2 (EC 3.1.3.48) (PTP2) OR PTP.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92115688; PubMed=1731319;
 RA "Moshiger B. Jr., Tillmann H., Westphal H., Tremblay M.L.; Cloning and characterization of a mouse cDNA encoding a cytoplasmic protein tyrosine phosphatase";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:499-503 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6N; TISSUE=Testis; and T-cell;
 RX MEDLINE=93140736; PubMed=1283199;
 RA Miyasaka H., Li S. L.;
 RA "Molecular cloning, nucleotide sequence and expression of a cDNA encoding an intracellular protein tyrosine phosphatase, PTPase-2, from mouse testis and T-cells";
 RT Mol. Cell. Biochem. 118:91-98 (1992)
 RN [3]
 RP TISSUE SPECIFICITY: protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE EXAMINED TISSUES. THE HIGHEST EXPRESSION LEVELS WERE FOUND IN OVARY, TESTES, THYMUS AND KIDNEYS. ALSO PRESENT IN SPLEEN, LIVER, HEART AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.


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CC
DR EMBL: L08863; NOT_ANNOTATED_CDS
DR PIR: A46289; A46289
DR PDB: 1AYB; 3I-AUG-94
DR PDB: 1AYB; 3I-AUG-94
DR PDB: 1AYB; 3I-AUG-94
DR PDB: 1AYB; 3I-AUG-94
DR MGI: 99511; PTPN11
DR InterPro: IPR000980; SH2
DR InterPro: IPR000987; TYR_phosphatase
DR InterPro: IPR00242; TYR_Proc_phphatase
DR Pfam: PF00017; SH2_2
DR Pfam: PF00102; Y_phosphatase_1
DR PRINTS: PR00700; PRYPHPHASE
DR PRINTS: PR00401; SH2DOMAIN
DR SMART: SM00194; PTPC_1
DR SMART: SM00252; SH2_2
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1
DR PROSITE: PS00564; TYR_PHOSPHATASE_2; 1
DR PROSITE: PS00564; TYR_PHOSPHATASE_PPC; 1
DR PROSITE: PS00011; SH2_2
DR HYPOLASS: SH2_2; SH2_2; Tyrosine phosphorylation; SH2 structure
FT DOMAIN 6 102 SH2_1
FT DOMAIN 112 216 SH2_2
FT DOMAIN 276 521 PROTEIN-TYROSINE PHOSPHATASE
FT ACCTIDE 463 463 BY SIMILARITY
SQ SEQUENCE 585 AA; 6662z MW: 67554.929488722a pI: 6.64
Query Match 5.1%; Score 13; DB 1; Length 585;
Best Local Similarity 100.0%; Pred No. 1; e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 179 GVVVHCASGIGR 191
DQ 457 GVVVHCASGIGR 469
RESULT 10
PTNH_HUMAN
ID PTNH_HUMAN STANDARD PRT 593 AA
AC Q06124
DT 01-FEB-1994 (Rel. 28, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE (Protein-tyrosine phosphatase, non-receptor type-11 (Pc-1; 3.13.48)
DE (Protein-tyrosine phosphatase,  $\alpha'$ ) (PTP- $\alpha'$ ) (SH-PTP) (SH-
DE PTP2) (SH-2).
GN PTPN11 OR PTP2; OR SHPTP2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Graziata; Vertebrata; Euteleostomi
OC Mammalia; Eularchia; Placentalia; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=umbilical cord;
RX MEDLINE-94120695; PubMed-781217;
RA Vogel W., Lambers F., Picot A.,
RT "Activation of a phosphotyrosine phosphatase by tyrosine
PT ph-phosphatase".
RL Science 259:1611-1614(1992)
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE-94106179; PubMed-1281790;

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RA Adachi M., Sekiya M., Miyachi T., Matsuda K., Hiroda Y., Imai K.,
RA Yachi A.;
RT "Molecular cloning of a novel protein tyrosine phosphatase SH-PTP2
RT with sequence similarity to the src-homology region 2."
RL PNAS Lett. 314:335-339(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-94029993; PubMed-8416283;
RA Hasten L., Ramachandran C., Liu S., Adam M.;
RT "Cloning, expression and mutational analysis of SH-PTP2, human
RT protein-tyrosine phosphatase."
RL Biochem Biophys Res Commun 196:124-133(1993).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-94087502; PubMed-1280823;
RA Freeman R.M., Jiri, Plutsky J., Neel B.G.;
RT "Identification of a human src homology 2-containing protein-tyrosine-
RT phosphatase: a putative homolog of Drosophila Cckcckrew."
RL Proc Natl Acad Sci U S A 89:11230-11234(1992).
RN [6]
RP PHOSPHORYLATION BY PDCFR.
RX MEDLINE-94106900; PubMed-8041791;
RA Bennett A.M., Tang T.L., Sugimoto S., Walsh C.T., Neel B.G.;
RT "Protein-tyrosine-phosphatase SHPTP2 couples platelet-derived growth
RT factor receptor beta to Ras."
RL Proc Natl Acad Sci U S A 91:7335-7339(1994).
RN [7]
RP Y-PAY CHYSEA LOCALIZATION (2.6 ANGSPONS) OF 1 526.
RX MEDLINE-98150850; PubMed-9491886;
RA Hol P., Plutsky S., Dhe-Paganon S., Eck M.J., Shewelson S.E.;
RT "Crystal structure of the tyrosine phosphatase SH-PTP2."
RL Cell 92:441-450(1998)
CC -1- FUNCTION: THIS PDCPSE ACTIVITY MAY DIRECTLY LINK GROWTH FACTOR
CC RECEPTORS AND OTHER SIGNALING PROTEINS THROUGH PROTEIN-TYROSINE
CC PHOSPHORYLATION. THE SH2 REGIONS MAY INTERACT WITH OTHER CELLULAR
CC COMPONENTS TO MODULATE ITS OWN PHOSPHATASE ACTIVITY AGAINST
CC INTERACTING SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HUMAN TISSUES:
CC PAPILLARY ABUNDANT IN HEART, BRAIN, AND SKELETAL MUSCLE.
CC -1- PTM: PHOSPHORYLATION OF TYR RESIDUES AT THE C-TERMINUS BY
CC PLATELET-DERIVED GROWTH FACTOR CREATES A BINDING SITE FOR THE SH2
CC DOMAIN OF GRB2.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. SUBCLASS THAT CONTAINS SH2 DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (see http://www.isb.slb.ch/annouce/
CC or send an email to license@lab.slb.ch)
CC
CC EMBL: L08863; NOT_ANNOTATED_CDS.
DR EMBL: X70766; CAA50045.1;
DR EMBL: D13540; BAA02740.2;
DR EMBL: L07527; AAA17052.1;
DR EMBL: L07535; AAA36611.1;
DR PIR: JN0805; JN0805.
DR PIR: 25HP; 16-FEB-99.
DR MIM: 176876;
DR InterPro: IPR000980; SH2.
DR InterPro: IPR000987; TYR_phosphatase.
DR InterPro: IPR00242; TYR_Proc_phphatase.
DR Pfam: PF00017; SH2_2.
DR Pfam: PF00102; Y_phosphatase_1.
DR PRINTS: PR00700; PRYPHPHASE.
DR PRINTS: PR00401; SH2DOMAIN.
DR SMART: SM00194; PTPC_1.

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SMART: SM00252; SH2; 2.
 CC PROSITE: PS00384; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 CC PROSITE: PS50001; SH2; 2.
 CC Hydrolyase; SH2 domain; Repeat: Phosphorylation; 3D-structure.
 CC DOMAIN 6 162 SH2 1.
 CC DOMAIN 112 216 SH2 2.
 CC ACT_SITE 276 517 PROTEIN-TYROSINE PHOSPHATASE.
 CC ACT_SITE 459 459
 CC MET_PESS 542 542 PHOSPHORYLATION (BY PROTEIN).
 CC MET_PESS 580 580 PHOSPHORYLATION (BY PROTEIN).
 CC CONFLICT 545 545 S - P (IN REF. 3).
 CC CONFLICT 548 548 S - P (IN REF. 3).
 CC SEQUENCE 593 AA; 68011 MW; 943856FA5E6C7445; CRC64;
 Query Match: 5.1%; Score 13; DB 1; Length 593;
 Best Local Similarity: 100.0%; Pred. No. 1; Le-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 179 GPVVHCSAGIGR 191
 453 GPVVHCSAGIGR 465
 RESULT 11
 FTIR KAT STANDARD; ERT: 593 AA.
 ID FENR KAT
 AC 641499; G62626;
 DI 01-NOV-1996 (Ref. 42; created)
 DI 15-JUL-1998 (Ref. 46; last sequence update)
 DI 16-OCT-2001 (Ref. 40; last annotation update)
 DE Protein tyrosine phosphatase, non-receptor type 11 (EC 3.1.3.48)
 DE (Protein tyrosine phosphatase SYP).
 DE FUNCTION:
 DE KATIN: non-receptor (KAT).
 DE Dikaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
 DE NBI TaxID 10116;
 CC STRAIN STRAIN: DAVLEY.
 CC STRAIN STRAIN: FROM N.A.
 CC MEDLINE 94125446; PubMed 7512964;
 CC MEDLINE 94125446; PubMed 7512964;
 CC "RNA splicing regulates the activity of a SH2 domain-containing
 CC protein tyrosine phosphatase.";
 CC J. Biol. Chem. 269:12534-12542(1994).
 CC [3]
 CC FACTIAL SEQUENCE:
 CC MEDLINE 94011127; PubMed 1062983;
 CC Huang A., Munkittrick J., Hata K., Szabo V., Szabo S.;
 CC "Purification and characterization of a rat liver protein-tyrosine
 CC phosphatase with sequence similarity to src homology region 2.";
 CC J. Biochem. 269:1395-200(1992).
 CC FUNCTION: THIS PHASE ACTIVITY MAY DIRECTLY LINK GROWTH FACTOR
 CC RECEPTORS AND OTHER SIGNALING PROTEINS THROUGH PROTEIN-TYROSINE
 CC PHOSPHORYLATION. THE SH2 REGION MAY INTERACT WITH OTHER CELLULAR
 CC COMPONENTS TO MODULATE ITS OWN PHOSPHATASE ACTIVITY AGAINST
 CC INTERACTING SUBSTRATES.
 CC CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein
 CC tyrosine + phosphate.
 CC SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC TERM PHOSPHORYLATION BY TYROSINE KINASES (BY SIMILARITY).
 CC SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-

CC TYROSINE PHOSPHATASE FAMILY, SUBCLASS THAT CONTAINS SH2 DOMAINS.
 CC -1 SIMILARITY: CONTAINS 2 SH2 DOMAINS.
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 CC or send an email to license@slb.slb.ch.
 CC EMBL: U09307; AAA20543.1;
 CC EMBL: U05963; AAA19131.1;
 CC PIR: S29281; S29281.
 CC HSP: P35235; IAYD.
 CC InterPro: IPR000980; SH2.
 CC InterPro: IPR000387; TYR_phosphatase.
 CC InterPro: IPR000242; Tyr_prot_phphase.
 CC Pfam: P00017; SH2; 2.
 CC Pfam: P00102; Y_phosphatase; 1.
 CC PRINTS: PR00700; PTYPHPRASE.
 CC PRINTS: PR00401; SH2DOMAIN.
 CC SMART: SM00194; PTPc; 1.
 CC SMART: SM00252; SH2; 2.
 CC PROSITE: PS00384; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 CC PROSITE: PS50001; SH2; 2.
 CC Hydrolyase; SH2 domain; Repeat: Phosphorylation.
 CC DOMAIN 6 102 SH2 1.
 CC DOMAIN 112 216 SH2 2.
 CC ACT_SITE 276 517 PROTEIN-TYROSINE PHOSPHATASE.
 CC ACT_SITE 459 459 BY SIMILARITY.
 CC CONFLICT 75 75 A -> P (IN REF. 1).
 CC CONFLICT 407 407 G -> GOLL (IN REF. 2).
 CC CONFLICT 547 547 Y -> S (IN REF. 2).
 CC SEQUENCE 593 AA; 68033 MW; 3129P10F0F60A48; CRC64;
 Query Match: 5.1%; Score 13; DB 1; Length 593;
 Best Local Similarity: 100.0%; Pred. No. 1; Le-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 179 GPVVHCSAGIGR 191
 453 GPVVHCSAGIGR 465
 RESULT 12
 FTIR KAT STANDARD; PRT: 989 AA.
 ID PTP3_DICDI
 AC P54637;
 DI 01-OCT-1996 (Ref. 34; created)
 DI 01-OCT-1996 (Ref. 34; last sequence update)
 DI 01-NOV-1997 (Ref. 35; last annotation update)
 DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (Protein tyrosine
 DE phosphate phosphatase 3) (EC 3.1.3.48) (Protein tyrosine
 DE (PTPc) OR PTP3) AND (PTPc2 OR PTP3).
 DE Dictyostelium discoideum (Slime mold).
 DE Dikaryota, Myxozozoa, Dictyostelida, Dictyostelium.
 DE NBI TaxID 44689;
 CC STRAIN STRAIN: DAVLEY.
 CC STRAIN STRAIN: FROM N.A.
 CC MEDLINE 36189156; PubMed 8628311;
 CC Gampert M., Howard P.K., Hunter T., Pittel R.A.;
 CC "Multiple roles of the novel protein tyrosine phosphatase PTP3 during
 CC Dictyostelium growth and development.";
 CC Mol. Cell. Biol. 16:2431-2444(1996).
 CC FUNCTION: SEEMS TO DEPHOSPHORYLATE A PROTEIN OF 130 KDa (P130).
 CC CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein
 CC tyrosine + phosphate.
 CC SUBCELLULAR LOCATION: Cytoplasmic.


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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCH_1axid-10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9534959; PubMed-755170;
RA Swales M., Berenstein E.H., Swalm W.D., Siraganian R.P.;
RT "Activation of IgE receptors in rat basophilic leukemia 2H3 cells
RT induces tyrosine phosphorylation of the cytosolic protein-tyrosine
RT phosphatase Hcyp1p."
RL J. Biol. Chem. 270:21902-21906(1995).
CC -! FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF T AND B LYMPHOCYTE
CC DEVELOPMENT AND SIGNAL TRANSDUCTION (BY SIMILARITY).
CC -! CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -! SUBCELLULAR LOCATION: cytoplasmic (by similarity)
CC -! SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC F001: U28456; AAA84443.1; -.
CC H001: H001; 1B2H.
CC DR InterPro: IPR006187; TYR_phosphatase.
CC DR InterPro: IPR006242; TYR_prol_phphatase.
CC DR Pfam: P400102; Y_phosphatase; 1.
CC DR PRINTS: PR00700; PRTYPHPTASE.
CC DR SMART: SM00194; PTPc; 1.
CC DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
CC DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
CC DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
CC KW hydrolase.
CC FT DOMAIN 119 342 PROTEIN TYROSINE PHOSPHATASE.
CC FT ACT_SITE 290 290 BY SIMILARITY.
CC SQ SEQUENCE 359 AA; 40314 MW; 5B98E196DB633677 CRC64;

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Query Match 3.94; Score 10; DB 1; Length 359;
Host Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 182 VVHCSAGIGR 191
DB 287 VVHCSAGIGR 296

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Search completed: June 18, 2002, 15:02:10
Job time: 115 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 15:00:15, Search time 26.52 seconds
(without alignments)
1656.890 Million cell updates/sec

Title: US-09-788-626-2

Perfect score: 254

Sequence: 1 DPCPRVAKIPKNNNNRVK

Scoring table:

Gapop 60.0, Gapext 60.0

Scoring table: 562222 seqs, 12291229 residues

Word size: 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: SP archaea:*

2: SP bacteria:*

3: SP fungi:*

4: SP human:*

5: SP invertebrate:*

6: SP mammal:*

7: SP mhc:*

8: SP organelle:*

9: SP phase:*

10: SP plant:*

11: SP rodent:*

12: SP virus:*

13: SP vertebrate:*

14: SP unclassified:*

15: SP virus:*

16: SP bacteriophage:*

17: SP archaea:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	50.0	414	4 Q9N004	Q9N004 homo sapien
2	54	21.3	62	13 Q96350	Q96350 gallus gall
3	43	16.9	272	11 Q99JST	Q99JST mus musculu
4	38	15.0	92	13 Q9YHE3	Q9YHE3 brachydanto
5	38	15.0	433	13 Q9P191	Q9P191 brachydanto
6	32	12.6	91	13 Q9YHE1	Q9YHE1 brachydanto
7	32	12.6	353	4 Q96A05	Q96A05 homo sapien
8	32	12.6	387	4 Q96H82	Q96H82 homo sapien
9	30	11.8	87	13 Q9HSC7	Q9HSC7 gallus gall
10	30	11.8	322	13 Q91B44	Q91B44 potamoxyg
11	30	11.8	406	11 Q922E7	Q922E7 mus musculu
12	16	6.3	379	13 Q9NKZ8	Q9NKZ8 epitalreus
13	16	6.3	548	5 Q9W031	Q9W031 drosophila
14	14	5.5	91	13 Q9YHE2	Q9YHE2 brachydanto
15	14	5.5	331	5 Q9N109	Q9N109 brachydanto
16	13	5.1	274	11 Q9W008	Q9W008 rattus norv

17	13	5.1	369	11 Q63419	Q63419 rattus norv
18	13	5.1	412	4 Q9NFK5	Q9NFK5 homo sapien
19	13	5.1	412	11 Q9Q0H9	Q9Q0H9 mus musculu
20	13	5.1	412	11 Q62695	Q62695 rattus norv
21	13	5.1	451	4 Q00342	Q00342 homo sapien
22	13	5.1	535	11 Q00817	Q00817 rattus norv
23	13	5.1	593	13 Q90887	Q90887 gallus gall
24	13	5.1	595	13 Q92144	Q92144 xenopus lae
25	13	5.1	597	11 Q64509	Q64509 mus musculu
26	13	5.1	656	11 Q62132	Q62132 mus musculu
27	13	5.1	657	4 Q15256	Q15256 homo sapien
28	12	4.7	63	13 Q90951	Q90951 gallus gall
29	12	4.7	121	4 Q9N0A7	Q9N0A7 homo sapien
30	12	4.7	694	13 Q91870	Q91870 xenopus lae
31	11	4.3	2460	11 Q64512	Q64512 mus musculu
32	11	4.3	2484	6 Q28906	Q28906 bos taurus
33	10	3.9	164	11 Q63848	Q63848 mus musculu
34	10	3.9	225	13 Q9N101	Q9N101 optarectus
35	10	3.9	229	5 Q9Y1W9	Q9Y1W9 corydactylus
36	10	3.9	241	13 Q9N103	Q9N103 optarectus
37	10	3.9	253	13 Q9N100	Q9N100 optarectus
38	10	3.9	275	5 Q9N110	Q9N110 optarectus
39	10	3.9	342	10 Q82710	Q82710 pisum sativ
40	10	3.9	338	10 Q82687	Q82687 gilycine max
41	10	3.9	342	13 Q91895	Q91895 potamoxyg
42	10	3.9	344	5 Q44901	Q44901 caenorhabdi
43	10	3.9	346	5 Q966M2	Q966M2 caenorhabdi
44	10	3.9	352	5 Q9BL74	Q9BL74 caenorhabdi
45	10	3.9	352	5 Q9XV04	Q9XV04 caenorhabdi

ALIGNMENTS

RESULT 1

Q9N004 PREHIMINARV; PRT; 414 AA.

Q9N004: 01-OCT-2000 (TREMBLrel. 15, created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE P0530115.1 (PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 (EC 3.1.3.48)) (FRAGMENT).

GN PTPN1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Placentalia; Hominidae; Homo.

NCBI_TaxID=9606;

RP 111

RF SOURCE: FROM N.A.

RA Wall M.

PL S:retrieved (MAP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL133230; CAC00618.1; -

DR HSSP: P18031; 1ppv.

DR InterPro: IPR000340; DS_phosphatase.

DR InterPro: IPR000387; TYR_PTPase.

DR InterPro: IPR00242; TYR_PTPase.

DR PRINTS: PR00700; PTP_PTPase.

DR SMART: SM00194; PTPC; 1.

DR PROSITE: PS00483; TYR_PHOSPHATASE_1; 1.

DR PROSITE: PS00566; TYR_PHOSPHATASE_2; 1.

DR PROSITE: PS00565; TYR_PHOSPHATASE_PTP; 1.

FM HYDROLASE; Receptor.

FT M_N_TER 1

SO SQUENGE 414 AA; 47464 MW; 323AACAA368A4556 CRC64;

Query Match: 50.0%; Score 127; DB 4; Length 414;

Best Local Similarity: 100.0%; Pred. No. 4; 8e-125;

Matches: 127; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 DPCPRVAKIPKNNNNRVKIDHNNINYNINASIIKMHFAQSYIIITGQNT. 60


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00 CYPRINIFORMES: Cyprinidae; Danio.
01 NCBI_TaxID=7955;
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MULTI-EXON PROTEIN TYROSINE PHOSPHATASE 2 (FRAGMENT).
 05 Gallus gallus (chicken).
 06 Eukaryotic Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 07 Actinopterygii: Atheri: Neoharpori: Galliformes: Phasianidae: Phasianidae:
 08 Gallus.
 09 NCBI TaxID 9041.
 10
 11
 12 SEQUENCE FROM N.A.
 13 MEDLINE 95224107; PubMed-7707864.
 14 Shook L.F., Dale D.J., Kline S.G., Maurer P.F.:
 15 "Protein Tyrosine Phosphatase Expressed in Developing Brain and
 16 Adult Muller Glia."
 17 Brain Res. Mol. Brain Res. 24:110-116(1995).
 18 HSSP: P18041; PPIV.
 19 InterPro: IPR000242; Tyr-prol-phosphatase.
 20 PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 21
 22 SEQUENCE: 87 AA; 9924 MW; 58E75506946638 CRC64.

Query Match 11.8%; Score 30; DB 13; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1, 5e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

143 HEHYTTPDGFVSPSPASFLNFKVRESG 172
 144 HEHYTTPDGFVSPSPASFLNFKVRESG 76

RESULT 10
 091004 PRELIMINARY: PRT: 322 AA.

01 OCT-2000 (TREMUR-rel. 15, Created)
 02 OCT-2000 (TREMUR-rel. 15, Last sequence update)
 03 DEC-2001 (TREMUR-rel. 19, Last annotation update)
 04 KPTPN3 PROTEIN (FRAGMENT).
 05 Putnam tyrosine motor (South American freshwater stingray).
 06 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Chondrichthyes:
 07 Elasmobranchii: Squali: Hypsogalea: Pristigaster: Batoidae:
 08 Myliobatiformes: Myliobatoidae: Potamorynidae: Potamorynidae.
 09 NCBI TaxID 66373.
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 12 SEQUENCE FROM N.A.
 13 MEDLINE 20219325; PubMed-10754074;
 14 Ono Koyanagi K., Suga H., Katoh K., Miyata T.:
 15 "Protein Tyrosine Phosphatases from Amphioxus, Hagfish, and Ray:
 16 divergence of tissue-specific isoform genes in the early evolution of
 17 vertebrates.".
 18 J. Mol. Evol. 50:402-411(2000).
 19 EMBL: AB034982; BAA05199.1; .
 20 HSSP: P18041; PTP.
 21 InterPro: IPR000387; Tyr-phosphatase.
 22 InterPro: IPR000242; Tyr-prol-phosphatase.
 23 InterPro: IPR000242; Tyr-prol-phosphatase.
 24 PRINTS: PR00700; PTPPHPTASE.
 25 SMART: SM00194; PTPC; 1.
 26 PROSITE: PS00048; TYR_PHOSPHATASE_1; 1.
 27 PROSITE: PS00055; TYR_PHOSPHATASE_2; 1.
 28 PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 29
 30
 31 SEQUENCE: 422 AA; 46964 MW; B004ED24E6F1197 CRC64;

Query Match 11.8%; Score 30; DB 13; Length 322;
 Best Local Similarity 100.0%; Pred. No. 4, 9e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

143 HEHYTTPDGFVSPSPASFLNFKVRESG 172
 144 HEHYTTPDGFVSPSPASFLNFKVRESG 102

RESULT 11
 0922E7 PRELIMINARY: PRT: 406 AA.
 01 DEC-2001 (TREMUR-rel. 19, Created)
 02 DEC-2001 (TREMUR-rel. 19, Last sequence update)
 03 DEC-2001 (TREMUR-rel. 19, Last annotation update)
 04 PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 2.
 05 Mus musculus (mouse).
 06 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 07 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
 08 NCBI TaxID-10090.
 09
 10
 11
 12 SEQUENCE FROM N.A.
 13 Strausberg R.:
 14 Submitted (MAY-2001) to the EMBL/GenBank/CCRF databases.
 15 EMBL: BC008269; AA008269.1; .
 16
 17 RECEPTOR.
 18
 19 SEQUENCE: 406 AA; 47460 MW; DFB881DF3C800D63 CRC64;

Query Match 11.8%; Score 30; DB 11; Length 406;
 Best Local Similarity 100.0%; Pred. No. 6e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

143 HEHYTTPDGFVSPSPASFLNFKVRESG 172
 144 HEHYTTPDGFVSPSPASFLNFKVRESG 203

RESULT 12
 09NKR28 PRELIMINARY: PRT: 379 AA.
 01 OCT-2000 (TREMUR-rel. 15, Created)
 02 OCT-2000 (TREMUR-rel. 15, Last sequence update)
 03 DEC-2001 (TREMUR-rel. 19, Last annotation update)
 04 HGTPTN3 PROTEIN (FRAGMENT).
 05 HGTPTN3.
 06 Epilatreus burgeri (Joshore hagfish).
 07 Eukaryota: Metazoa: Chordata: Craniata: Hyperotreti: Myxiniiformes:
 08 Myxiniidae: Eptacrinidae: Eptacrinus.
 09 NCBI TaxID-7764.
 10
 11
 12 SEQUENCE FROM N.A.
 13 MEDLINE-20219325; PubMed-10754074;
 14 Ono Koyanagi K., Suga H., Katoh K., Miyata T.:
 15 "Protein Tyrosine Phosphatases from Amphioxus, Hagfish, and Ray:
 16 divergence of tissue-specific isoform genes in the early evolution of
 17 vertebrates.".
 18 J. Mol. Evol. 50:402-411(2000).
 19 EMBL: AB034579; BAA95186.1; .
 20 HSSP: P18031; 2HNO.
 21 InterPro: IPR000387; Tyr-phosphatase.
 22 InterPro: IPR000387; Tyr-phosphatase.
 23 InterPro: IPR000242; Tyr-prol-phosphatase.
 24 PRINTS: PR00700; PTPPHPTASE.
 25 SMART: SM00194; PTPC; 1.
 26 PROSITE: PS00048; TYR_PHOSPHATASE_1; 1.
 27 PROSITE: PS00055; TYR_PHOSPHATASE_2; 1.
 28 PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 29
 30
 31 SEQUENCE: 379 AA; 42672 MW; A2493B3F3090174 CRC64;

Query Match 6.8%; Score 16; DB 13; Length 379;
 Best Local Similarity 100.0%; Pred. No. 3, 1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

R1 phosphatase sub families.
 R1 Submited (Oct 1998) to the EMBL/Genbank/DBJ databases.
 R1 EMBL: AF097482; AAC9748.1;
 R1 HSSP: P18041; 1PTV
 R1 InterPro: IPR002442; Tyr prot phosphatase.
 R1 PRINSE: PR00700; PRY069458.
 R1 PROSITE: PS50055; TYR PHOSPHATASE_PP3_1.
 R1 Hydrolyase.
 R1 NON TER 1 1
 R1 NON TER 91 91
 R1 SEQUENCE 91 AA: 10444 MW: 8428676.486741 CRC64:

Query Match %:98; Score 14; DB 14; Length 91;
 Local Local Similarity 100.0%; Pred. No. 1; E-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 149 WIPPEWIPESHASHL 162
 149 WIPPEWIPESHASHL 69

RESULT 15

Q9N109 PRELIMINARY DB: 341 AA.

Q9N109 01 OCT 2000 (TREMUR) 15; Created

Q9N109 01 OCT 2000 (TREMUR) 15; Last sequence update

Q9N109 01 DEC 2001 (TREMUR) 15; Last annotation update

Q9N109 AMPININ PROTEIN (PRACININ).

Q9N109 AMPININ.

Q9N109 Branchiostoma belcheri (Amphioxus).

Q9N109 Eukariotid; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

Q9N109 Branchiostoma.

Q9N109 NCBI TaxID 7741;

Q9N109 113

Q9N109 SEQUENCE FROM N.A.

Q9N109 MEDLINE 20219425; PubMed 10754074;

Q9N109 Yano Koyanagi K.; Suga H.; Katoh K.; Miyata T.;

Q9N109 "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:

Q9N109 divergence of tissue specific isoform genes in the early evolution of

Q9N109 vertebrates.";

Q9N109 J. Mol. Evol. 50: 402-411 (2000).

Q9N109 EMBL: AM035646; AAC96175.1;

Q9N109 HSSP: P18041; 2HNO.

Q9N109 InterPro: IPR000487; Tyr phosphatase.

Q9N109 InterPro: IPR000442; Tyr prot phosphatase.

Q9N109 PRINSE: PR00700; PRY069458.

Q9N109 SMART: SM00194; Pfam: 1.

Q9N109 PROSITE: PS00484; TYR PHOSPHATASE_1; 1.

Q9N109 PROSITE: PS50056; TYR PHOSPHATASE_2; 1.

Q9N109 PROSITE: PS50055; TYR PHOSPHATASE_PP3_1.

Q9N109 Hydrolyase.

Q9N109 NON TER 1 1

Q9N109 NON TER 91 91

Q9N109 SEQUENCE 91 AA: 98450 MW: 4148736.709459 CRC64:

Query Match %:98; Score 14; DB 14; Length 91;
 Local Local Similarity 100.0%; Pred. No. 1; E-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 249 WIPPEWIPESHASHL 248
 249 WIPPEWIPESHASHL 162

Search completed: June 18, 2002, 15:01:54
 Job time: 98 sec